

FIGURE 1

AGGCGGGCAGCAGCTGCAGGCTGACCTTGACGCTTGGCGGAATGACTGGCCTCACAACTGCTGTTTCTT
CTTACCATTTCCATCTTCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG
GCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTACGGATGAAACCGTATGCCC
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG
AGAAAGTGTGAGGTCAACTTGACGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT
CAACCACGACCCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACC
CCTTCACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCGC
CTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG
CACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCCGAGACCATCCTCCTTGACCTTT
GTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

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FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKQGGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA
QLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRI PVDLPEARCLCLGCVNPFTMQEDRSMVSVP
VFSQVPVRRRLCPPPPRTGPCRQRAVMETI AVGCTCIF

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FIGURE 3

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCCCGGCCTCC
TGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC
GGTACCCACACTGCTACTCGGCTGAGGAACTGCCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGG
TGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCGGTGCTGCGGCCGAGGAGGTGTTGGAGGCAGACACCCAC
CAGCGCTCCATCTCACCCCTGGAGATAACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT
CGCCGAGTGCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC
GGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGGCTCCCCACACCT
GGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGCTGCACCTGCGTGCTGCCCCGTTCAGT
GTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGGCACCCCCTATTTATGTG
TATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTGCTCCCGGCTTCCCT
TACCCTATCACTGGCCTCAGGCCCGCAGGCTGCCTCTTCCCAACCTCCTTGAAGTACCCCTGTTTCTTA
ACAATTATTTAAGTGTACGTGTATTATTAACTGATGAACACATCCCCAAAA

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FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGQALPVALVSSLE
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYFPQKLAFAECLCRGCIDARTGRE
TAALNSVRLQLSLLVLRRLRRPCSRDGSGLPTPGAFAFHTEFIHVPGCTCVLPRSV

Signal peptide:	Amino acids 1-18
Tyrosine kinase phosphorylation site:	Amino acids 112-121
N-myristoylation sites:	Amino acids 32-38;55-61;133-139
Leucine zipper pattern:	Amino acids 3-25
Homologous region to IL-17:	Amino acids 99-195

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GCGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCACTCA
GTGCCCCGACTTGTGACTGAGTGTGCAGTGCCCGAGCATGTACCAGGTCACTGCAGAGGGCTGCCTGAGGGCT
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG
GGGCCAAGTGAGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGATGAGGGGAGCGACCCAGATTAGGTGA
GGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCATTCTTGGCAATGGTCATGGGAACCCACACCT
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGA
CCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGCTCCCCCAGGA
CCTGTACCACGCCCGTTGCCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCATATGGACCCCCGGG
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCC
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGTGCGGCCCCGTGT
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG
CCATGAAGGGCCAGGATGCCAGATGCTTGGCCCCCTGTGAAGTGCTGTCTGGAGCAGCAGGATCCCGGGAC
AGGATGGGGGGCTTTGGGGAAAACCTGCACCTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC
CGGAAGCTGGTGTCTGTCAATTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCATTTCTGGAGGCCACCA
CTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACTTTCTAGATATTTCCCC
CTTGCTGGAGAAGAAAGAGCCCCTGGTTTTATTTGTTTGTCTTACTCATCACTCAGTGAGCATCTACTTTGG
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA
GAGATTTTATCCAAATAAAATATCTTTATTTAAAAATGAAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPARPNRHP
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR
RPCHGEKGTGTHKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide:

Amino acids 1-32

N-glycosylation site:

Amino acids 136-140

Tyrosine kinase phosphorylation site:

Amino acids 127-135

N-myristoylation sites:

Amino acids 44-50;150-156

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FIGURE 7

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCCAGGGCGGGCAGGCG
CCCCGCGCGGGCCGCGGGGCTGCGCGGACCGGCCGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG
CCGGCGTGCTCAGTGCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC
CCGGCAGGGGGCAGGCCCGGCGACCGCCGCTTCCGGCCGCCACCAACCTGCGCAGCGTGTGCGCCTGGGC
CTACAGAATCTCCTACGACCCGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCGGGGCT
GCCTGACCGGGCTGTTGCGCGAGGAGGACGTGCGCTTCCGCAGCGCCCCTGTCTACATGCCACCGTCTGC
CTGCGCCGCACCCCCGCTGCGCCGCGGCGCTTCCGTCTACACCGAGGCCTACGTACCATCCCCGTGGG
CTGCACCTGCGTCCCCGAGCCGGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGAGGCCGGTCTGCCCCGGGAGGTCTCCCCGG
CCCGCATCCCAGGCGCCCAAGCTGGAGCCGCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGCACC
GAGCAAACCAAGTGCCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGCTGGAAGCTGATGGGAAACGACCCGGCACGG
GCATCCTGTGTGCGGCCCGCATGGAGGGTTTGGAAGGTTACGGAGGCTCCCTGAGGAGCCTCTCAGATC
GGCTGCTGCGGTGCAGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT
AAAGCAATCTAAAAATAATAAAGTATAGCGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGA
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTTGTAGCTGGTACACTCTGG
CCTGGGTCTCTGAATTCAGCCTGTCAACGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC
TTCCTTCCACTGAAGTCTTCACGGGCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCA
GGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGC
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGGA
ACGTGACATCTTTGCCAGTTGTGAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAAGAGGCTTGCTGAAGGAT

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FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC
PAGGRPGRRRFRPPTNLRVSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGEEDVRFERSAPVYMP TVV
LR RTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQAKLLLGPNDAPAGP

Signal peptide:

Amino acids 1-15

N-glycosylation sites:

Amino acids 68-72;181-185

Tyrosine kinase phosphorylation site:

Amino acids 97-106

N-myristoylation sites:

Amino acids 17-23;49-55;74-80;
118-124

Amidation site:

Amino acids 21-25

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FIGURE 9

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCAT
GGTCAAGTACTTGCTGCTGTCGATATTGGGGCTTGCCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACCTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACCTGG
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCTGGTGACTGTTGGCTGCACCTG
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

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FIGURE 10

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS
RNIESRSTSPWNYTWTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

Amino acids 1-30

N-glycosylation site:

Amino acids 83-86

N-myristoylation sites:

Amino acids 106-111;136-141

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FIGURE 11

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGAGACTTGA
GGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAAGATTGTGTGACGGGCAAAGCAA
CTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCTTCCAGACTCAGACCAGACCTCTGGTG
GTAAATGGACATTTTCTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATGGGGCCATAAT
ATTCTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA
CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTA
AGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACACCACTCCCCTGGGAAACAGATACATGGCTCTTATC
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGACAGTCACTCCATATTTTCTACTTGTGGCA
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCTGGATAAC
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC
CCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA
TTTCTTCAAACCATTCAGAAAGTGAGGTATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGG
TCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTCCAATGACGTCA
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC
CTTGCCTTTAAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCTCTGCACAAATACGTGGTGGTCTACTT
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAAGCCTGC
CACGATGGCTGCTGCTCCTTGTAG

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FIGURE 12

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRLDLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVFPFLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKTSEFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGFPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
GCCSL

Signal sequence:	Amino acids 1-14
Transmembrane domain:	Amino acids 290-309
N-glycosylation sites:	Amino acids 67-70;103-106;156-159; 183-186;197-200;283-286
cAMP- and cGMP-dependent protein kinase phosphorylation sites:	Amino acids 228-231;319-322
N-myristoylation site:	Amino acids 116-121
Amidation site:	Amino acids 488-491

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FIGURE 13

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG
AGTGCACAACTACCCAGCACAGCCCCCTCCGCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCTGCCA
CCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGCAGCACAGGGCCTCAGGCCTGGGT
GCCACCTGGCACCTAGAAAGATGCCTGTGCCCTGGTTCTTGCTGTCTTGGCACTGGGCCGAAGCCCAGTGG
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCTCTCCTGCCGCTC
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCTGCTCCGGGCCCCGTGCTGGCGCCTACGCA
CCTGCAGACAGAGCTGGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCCTACTGCCCC
CTGCGTCTGTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCTTACTCAGCCCAGGTACGAGAAGGA
ACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTCAGCAGATGGTGACAACGTGCATC
TGTTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCTGTACTGGAATCAGGTCCAGGGCCCCCA
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG
CCTCTGTATTTCAGGTGTGGCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACC
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC
GCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT
GGTCCCACCGCTTTCCTGGGAGAAGCTCACTGTGGACAAGGTTCTCGAGTTCCTATTGCTGAAAGGCCACC
CTAACCTCTGTGTTTCAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGTGTTGGGCTGACTCCCTG
GGGCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTT
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGECCTGCCTACTCTTTGCCGCTGCGCTTTC
CCTCATCTCTCTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAACAGGACGTCCGCTCGG
GGGCGGCCGCCAGGGGCCGCGCGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG
GGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTCTGAACT
GAGCGCGCAGGGGCCCTGGCTTGGTTTCACGCGCAGCGGCGCCAGACCCTGCAGGAGGGCGGCGTGGTG
TCTTGCTCTTCTCTCCCGTGCGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCCGG
GCGCACGGCCCGCACGACGCTTCCGCGCCTCGCTCAGCTGCGTGTGCCCCACTTCTTGAGGGCCGGG
GCCCCGCGAGCTACGTGGGGCCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCA
CCGTGCCCGTCTTCACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCG
CGTTCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCGGGGCCCTTCAGCCAGCCCTGGATAGCTACTT
CCATCCCCCGGGGACTCCCGCGCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGACGGGA
CTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 14

MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWDS DILCLPGDIVPAPGPVLAPTHLQTELV
 LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
 QVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNV SADGDNVHLVLNV
 EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN
 LWQAARLRLTLQSWLLDAPCSLPAAEALCWRA PGGDPCLVPPLSWENVTVDKVLEFP LLKGHPNLCVQ
 VNSSEKLQLOECLWADSLGFLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYLLQDLQS
 GQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALS LILLKKDHAKGWLRLKQDVRS GAAARG
 RAALLLYSADD SGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFWHAQRRTLQEGGVVLLFSP
 GAVALCSEWLQDGVSGPGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFT
 LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPGTPAPGRGVGPGAGPGAGDGT

signal sequence: Amino acids 1-20

transmembrane domain: Amino acids 453-473

N-glycosylation sites: Amino acids 118-121;186-189;198-201;
 211-214;238-241;248-251;334-337;
 357-360;391-394

Glycosaminoglycan attachment site: Amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site:
 Amino acids 552-555

N-myristoylation sites: Amino acids 107-112;152-157;319-324;
 438-443;516-521;612-617;692-697;
 696-701;700-705

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FIGURE 15

CGAGGGCTCCTGCTGGTACTGTGTTGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCC**ATG**GGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTTCGCCACCTGCCCCACTGGAACACC
CGCTGTCTCTGGCCTCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCCCGCTGTTTGTGCCAGCATCTGC
TGTCAGGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAGTCTTCCACA
TTCAAGTTCTATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTACCTGTCTC
TGAGAAGAGCCATCACATTTCCATCCCCCTCCCCAGACATCTCCACAAAGGGACTTCGCTCTAAAAGGACCC
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACAAAGGCATGGAGGACCCGAGTTT
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCCGGGTGACCATATCTTCAGGCCCTGAGGTGAGCGTGCG
TCTTTGTACCAAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG
GGGGCCACACTGTAGAGCTGCCTTATGAATTCCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAA
GAGGACACTGTGAGGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA
GTCAGTGCACCTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCACTGA
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATAACCCTTTGCAAAGACCTCCCGAATGCCACGGCT
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCAGCTCTGCTTCAAGTTCTCTTT
TGAAAACAGCAGCCATGTTGAATGCCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCAGTGCTGCCTGGAGCCTC
CCAGGCTTGGGGCAGGACACTTTGGTGCCCCCGTGTACACTGTGAGCCAGGCCCGGGGCTCAAGCCAGT
GTCCTAGACCTCATCATTCCTTCTGAGGCCAGGTGCTGTGTCTGGTGTGGCGGTGAGATGTCCAGT
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG
GCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTCAGGCCCGGGCCAGC
GCGGCCAGTGCTCCTCCTGCACGCGCGGACTCGGAGGCGCAGCGCGCCTGGTGGGAGCGCTGGCTGAAC
TGCTACGGGCAGCGCTGGGCGGCGGCGGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT
GGGCCCCGCTGCCGTGGCTCTGGGCGGCGGCGGACGCGCGTAGCGCGGAGCAGGGCACTGTGCTGCTGCTGT
GGAGCGGCGCCGACCTTCGCCCCGTGAGCGGCCCCGACCCCCGCGCGCGCCCTGCTCGCCCTGCTCCAC
GCTGCCCCGCGCCCGCTGCTGCTGCTCGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC
GCTGCGCGCCCTGCCGCGCTACCGCCTGCTGCGCGACCTGCCGCGTCTGCTGCGGGCGCTGGACGCGCGGC
CTTTCGCAGAGGCCACCAGCTGGGGCGCCTTGGGGCGCGGCGAGCGCAGGCAGAGCCGCTAGAGCTGTGC
AGCCGGCTTGAACGAGAGGCCCGCCGACTTGACAGCCTAGGTTGAGCAGAGCTCCACCGAGTCCCGGGTGTCT

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FIGURE 16

MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSTGSSAYIPCRTWWALFSTKPWCV
RVWHCSRCLCQHLLSGGSLQRGLFHLVQKSKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS
PDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH
TQMVMALTLCPLKLEAALCQRHDWHTLCKDLNPATARES DGWYVLEKVDLHPQLCFKFSFGNSSHVECPH
QTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR
PGCCVLVWRSDVQFAWKHLLCPDVSYRHLGLLILALLALLTLLGVVLALT CRRPQSGPGPARPVLLLHAAD
SEAQRRLVGALAELLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLWLGADLRPVS
GPDPRAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLLRALDARPF AEATSWGR
L GARQRRQSRLELC SRLERE AARLADLG

Signal peptide: Amino acids 1-23

Transmembrane domain: Amino acids 455-472

N-glycosylation sites: Amino acids 318-322; 347-351; 364-368

Glycosaminoglycan attachment site: Amino acids 482-486

cAMP- and cGMP-dependent protein kinase phosphorylation sites:
Amino acids 104-108; 645-649

Tyrosine kinase phosphorylation site: Amino acids 322-329

N-myristoylation sites: Amino acids 90-96; 358-364; 470-476

Eukaryotic cobalamin-binding proteins: Amino acids 453-462

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FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGGAGTGGGGGAGGTCAGACGGGGCGGTTGGAGGGGGAGGGAT
GCCACGCGCTTCTGCCTCAGGTGTTCTGCGTTGTTTGTTCAGTGGAGAGCAGGGAGTGGGGCCAGCCAGCA
GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGGAAG
CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT
TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCTGAAAGGATTTGGGTAATACTGGAGGAGCTGAAGT
CGGAGGGAAGACAGTGCCAACAACCTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGT
GGAATGGAATCTCAACCTTTCTGAAATATGAAATTTGAAACGGATTATTTTCGTAAAGGTTGTCCCTTTTCC
TTCCATTAAAAACGAAAGCAATTACCACCCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC
CGGACAATCTAGCTTGTAACCCCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC
AGGTGTCTTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCTTCGACCACGCACCGCACAACTTC
GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAAGCGAAAGACCTGTAAGCA
GGAGCAAACCTACAGAGATGACCAGCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG
TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCCTTAAAGCCAGTGCACCTCCCCGTGGGCCGGG
CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCGCGACGCTCTTCACTGTGAT
GTGCCGCAAGAAGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA
CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCCGCGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGC
CAGAATCACATGAATGTCGTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT
GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTATCCAGAAGATCCACGAGT
CCCAGTTCATCATTTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA
GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTCTTCTGTTGGCGGTGTGAGCCATTGCCGAAAAGCTCCG
CCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCTGCGAGG
GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCC
CACCTGCACTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAATA
CTTCGGGAGCAAGTCAGGCCGCTCCCTATACGTCGCCATTTGCAACATGCACCAGTTTATTGACGAGGAGC
CCGACTGGTTTCGAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAG
AAATTTGATTTCGGGCTTGGTTTAAATGATGTGATGTGCAACCAGGGCCTGAGAGTGACTTCTGCCTAAA
GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAAGCATGGGGGCCTGG
ACCAAGACGGGGAGGCCCGGCTGCCCTTGACGGTAGCGCGCCCTGCAACCCCTGCTGCACACGGTGAAA
GCCGGCAGCCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC
TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCTCCT
CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCTTCCAAGCTCCTCTCTTCTGGGTGATGCAAAGCA
GATCTTGGTTGCCGAGCTACACTGATGAACTCCACGCGGTGCCCCCTTTGTAACAAAACGAAAGAGTCTA
AGCATTGCCACTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 18

MPRASASGVPALFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT
 ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
 PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN
 FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA
 GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD
 GQNHMNVVQCFAYFLQDFCGCEVALDLWEDESLCREGQREWVIQKIHESQFIIIVCSKGMKYFVDKKNYKH
 KGGGRGSGKGELFLVAVSAIAEKLQAKQSSSAALSKFIAVYFDYSCEGDVPGILDSTKYRLMDNLPQLC
 SHLHSRDHGLQEPGQHTRQGSRRNYFRSKSGRSLYAICNMHQFIDEEDWFEKQFVFPFPPFLRYREPV
 EKFDGLVLDVDMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGMGLDQDGEARPALDGSAAALQPLLHTV
 KAGSPSDMPRDSGIYDSSVPSELSPPLMEGLSTDQTETSSLTESVSSSSSGLGEEPPALPSKLLSSGSCK
 ADLGCRSYTDELHAVAPL

Transmembrane domain:

Amino acids 283-307

N-glycosylation sites:

Amino acids 31-34;38-41;56-59;
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:

Amino acids 232-235

Tyrosine kinase phosphorylation sites: Amino acids 312-319;416-424

N-myristoylation site:

Amino acids 19-24;375-380;428-433;
429-434;432-437;517-522;574-579;
652-657;707-712

FOOEE" 45FOOQ"

FIGURE 19

h-IL17 1 - - - - - MTPGKTSLVSL L L L S L E A I V K A G I T I P R
 h-IL17B 1 - - - - - MDWPHNLLFLLTISIFLG LGOPRSPKSKRKGGGR P G P L A P G P
 h-IL17C 1 M T L L P G L L F L T W L H T C L A H D P S L R G H P K S H G T P H C Y S A E E L P L G O A P P H
 h-IL17D 1 - - - - - M L V A G F L L A L P P S W A A G A P R A G R R P A R P R G C A D R P
 h-IL17E 1 - - - - - M R E R P R L G E D S S L I S L F L Q V V A F L A M V M G T H T Y S H
 h-IL17F 1 - - - - - M T V K T L H G P A M V K Y L L L S I L G L A F L S E A A A R K I P K V G

 h-IL17 30 N P G C P N S E D K N F P R T V M V N L N I H N R N T N T N P K - - - - - R S S D
 h-IL17B 43 H Q V P L D L V S R M K P Y A R M E E Y E R N I E E M V A Q L R N S S E L A Q R K C E V N L Q L W M
 h-IL17C 51 L L A R G A K W G O A L P V A L V S S L E A A S H R G R H E R P S A T T O C P V L R P E E V L E A D
 h-IL17D 36 E E L L E Q L Y G R L A A G V L S A F K H T L Q L G P R E Q A R N A S C P A G G R P A D R R F R P P
 h-IL17E 36 W P S C C P S K G O D T S E E L L A W S T V P V P P L E P A R P N R H P E S C R A S - - - - - E D G P
 h-IL17F 38 H T F F Q K P E S C P P V P G G S M K L D I G I I N E N Q R V S - - - - - M S R N

 h-IL17 66 Y Y N R S T S P W N L H R N E O P E R Y P S V I W E A K C R H L G C I N A D - G N V D Y H M N S V P
 h-IL17B 93 S N K R S L S P W G Y S I N H O P S R I P V D L P E A R C L C L G C V N P F T M O E D R S M V S V P
 h-IL17C 101 T H Q R S I S P W R Y R V D T O E D R Y P Q K L A F A E C L C R G C I D A R T G R E T A A L N S V R
 h-IL17D 86 T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y C L C R G C L T G L F G E E D V R F R S A P
 h-IL17E 82 L N S R A I S P W R Y E L O R O L N R L P O D L Y H A R C L C P H C V S L O T G S H M D P R G N S E
 h-IL17F 74 I E S R S T S P W N Y T V T W D P N R Y P S E V V Q A Q C R N L G C I N A O - G K E D I S M N S V P

 h-IL17 115 I Q Q E L L V L R R E - - - - - P P H C P N S F P L E K I L V S V G C T C V T P I V H H V A
 h-IL17B 143 V F S Q V P V R R R L C P P P - - - - - P R T G P C R O R A V M E T I A V G C T C I F - - -
 h-IL17C 151 L L Q S L L V L R R R P C S P D G S G L P T P G A F A F H T E F I H V P V G C T C V L P R S V -
 h-IL17D 136 V Y M P T V L L R R T P A C A G - - - - - G R S V Y T E A Y V T I P V G C T C V P E P E K D A D
 h-IL17E 132 L L Y H N Q T V F Y R R P C H G E K - - - - - G T H K G Y C L E R R L Y R V S L A C V C V R P R V M G -
 h-IL17F 123 I Q Q E T L V V R R K - - - - - H Q G C S V S F O L E K V L V T V G C T C V T P V I H H V O

 h-IL17D 179 S I N S S I O K Q G A K L L L G P N D A P A G P X

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FIGURE 20

IL17B distribution

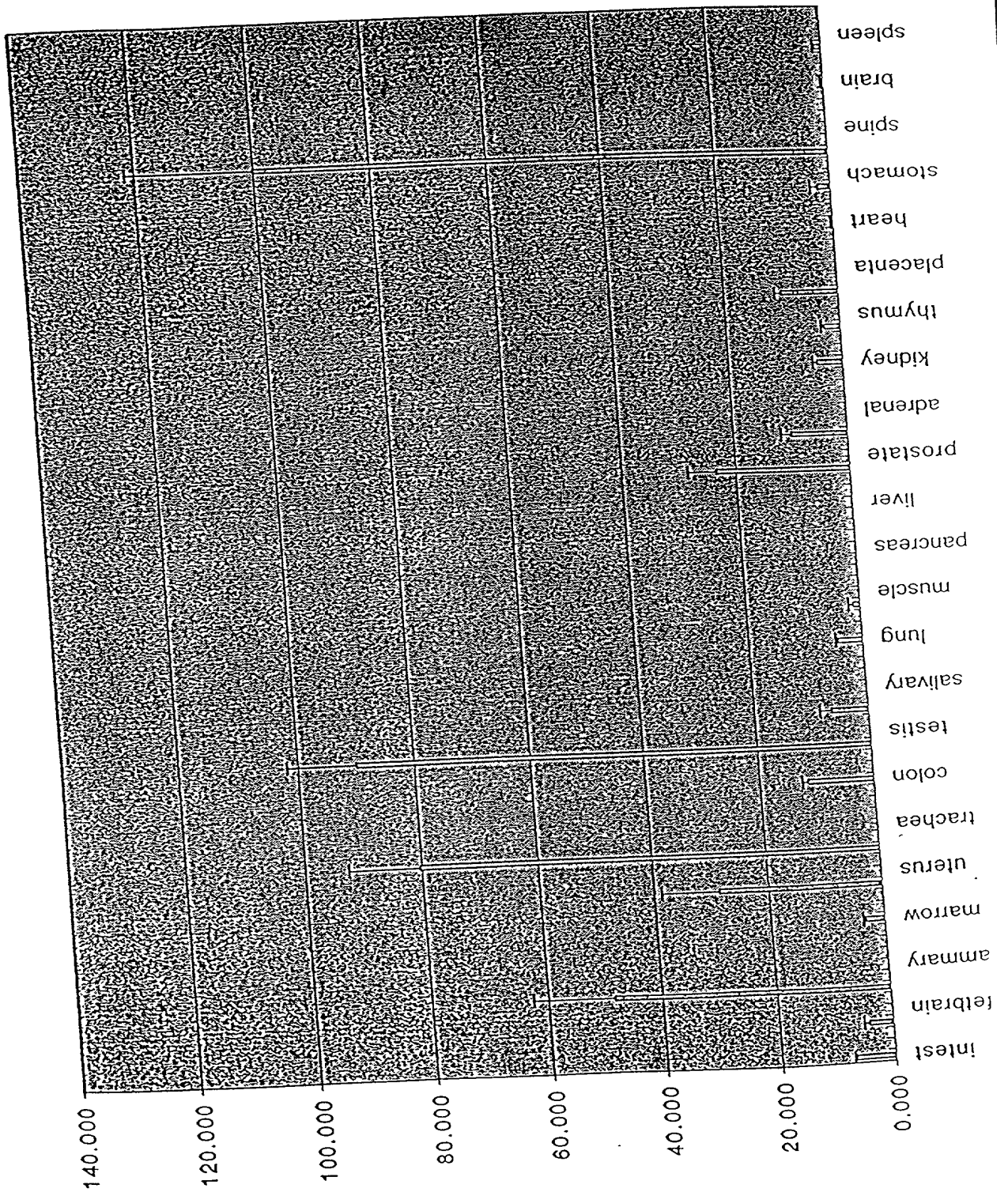
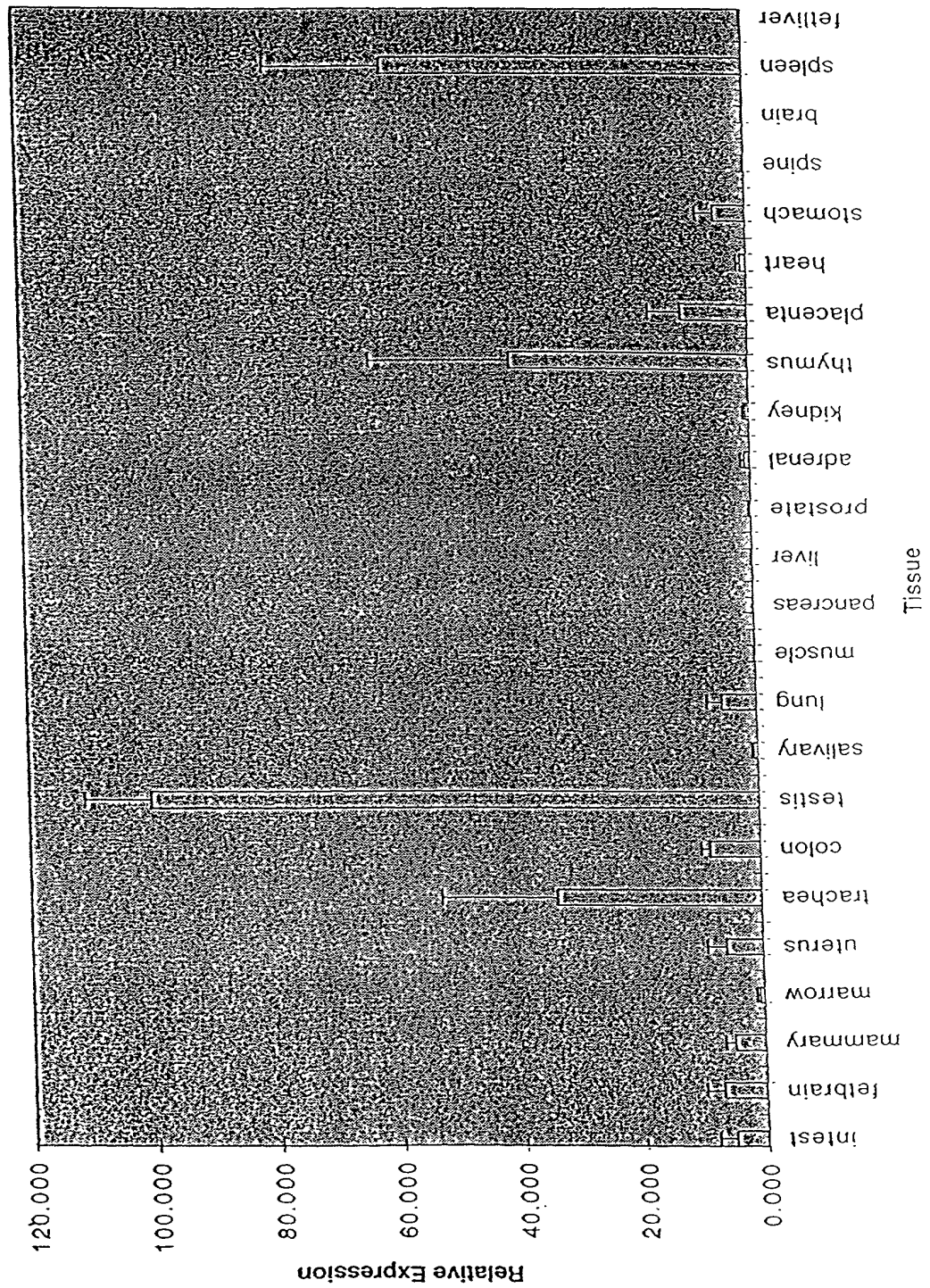


FIGURE 21

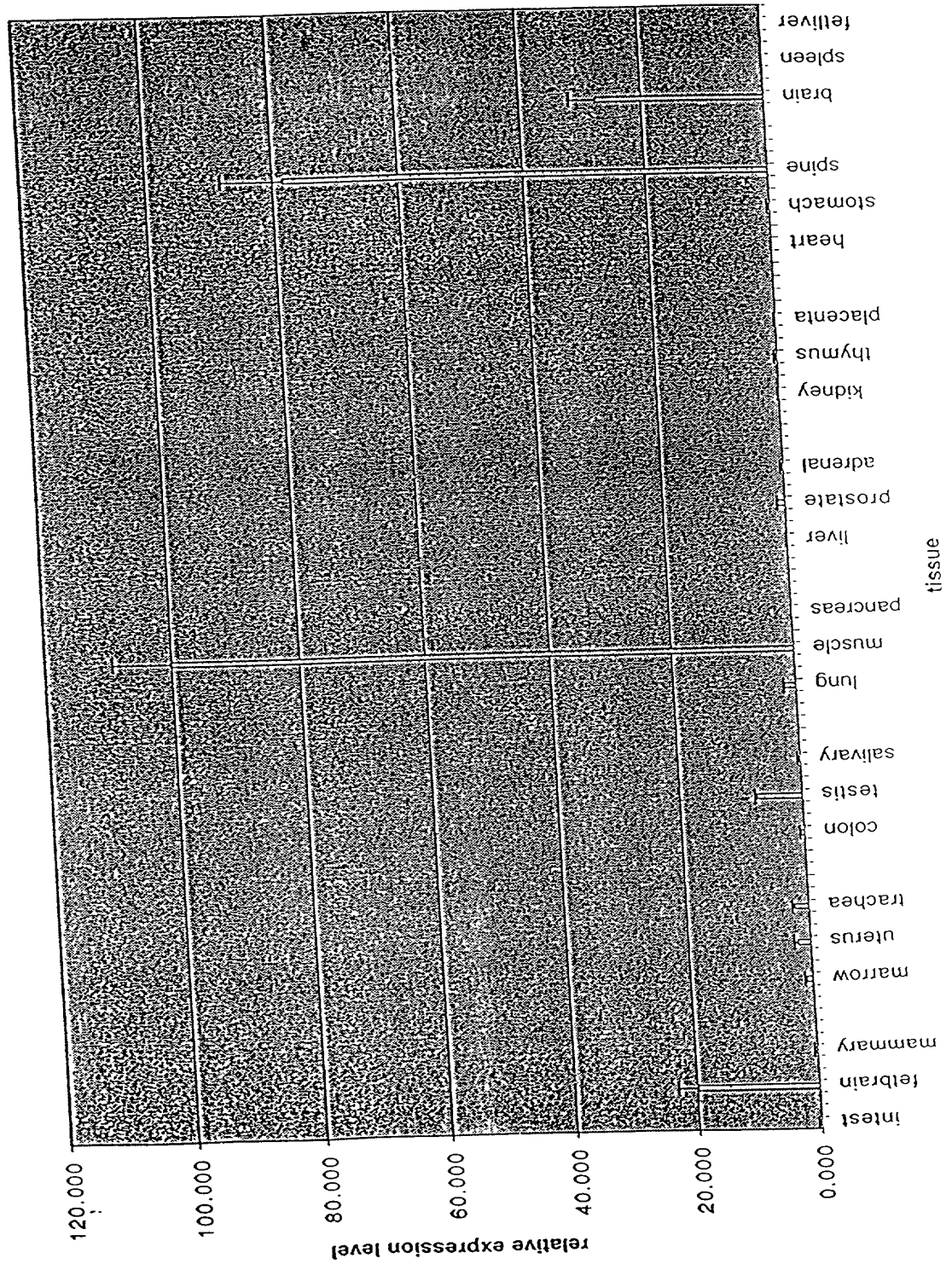
IL17C Distribution



T00E0T / S10000T

FIGURE 22

IL17D Distribution



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FIGURE 23

"TOOBT" /STOODT

Brain	
heart	
kidney	
liver	
lung	
colon	
marrow	
intestine	
spleen	
stomach	
thymus	
prostate	
muscle	
testis	
uterus	
fetal brain	
fetal liver	
spinal chord	
placenta	
adrenal	
pancreas	
salivary	
trachea	
mammary	

FIGURE 24

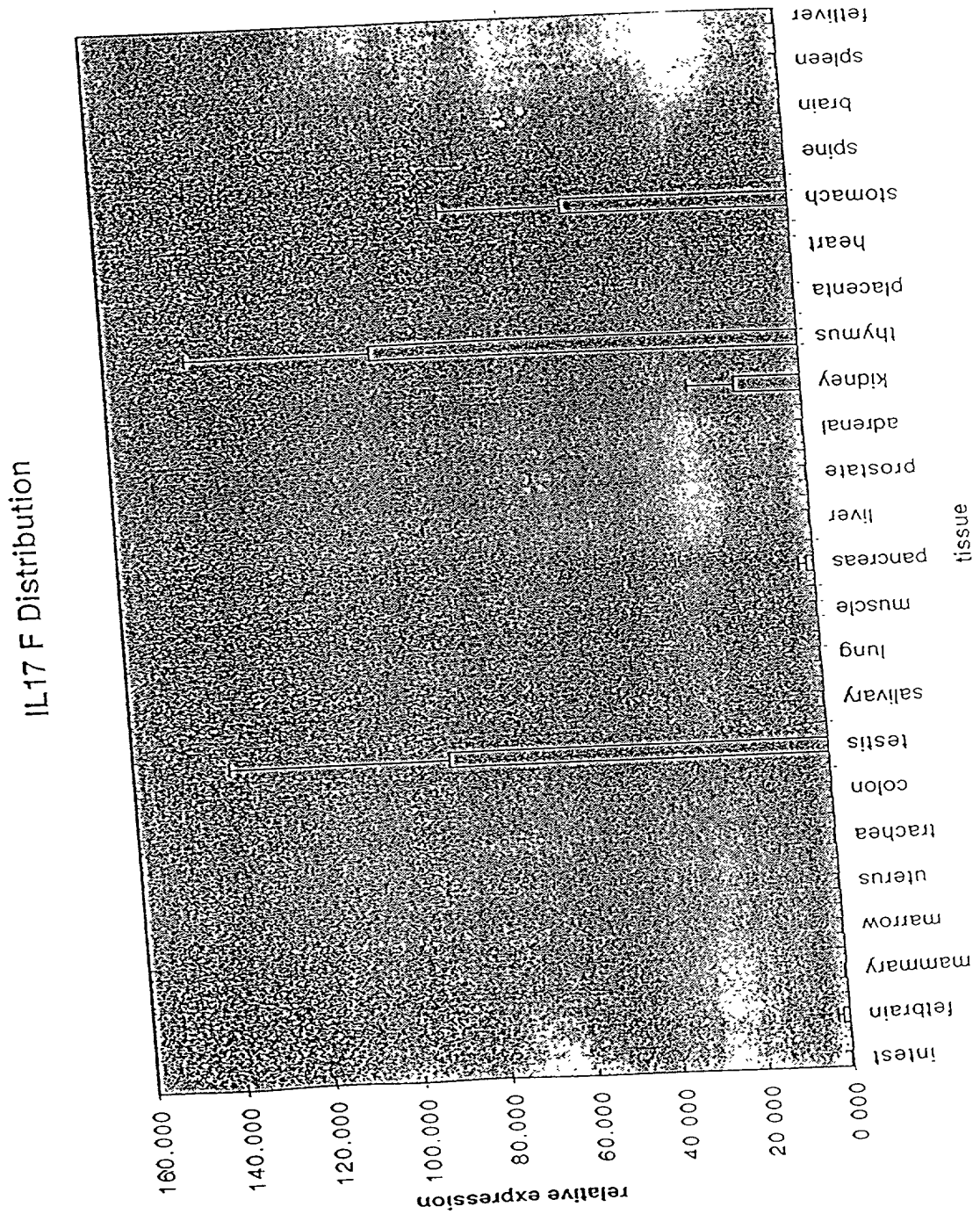


FIGURE 25

IL17Rhom-1 Distribution

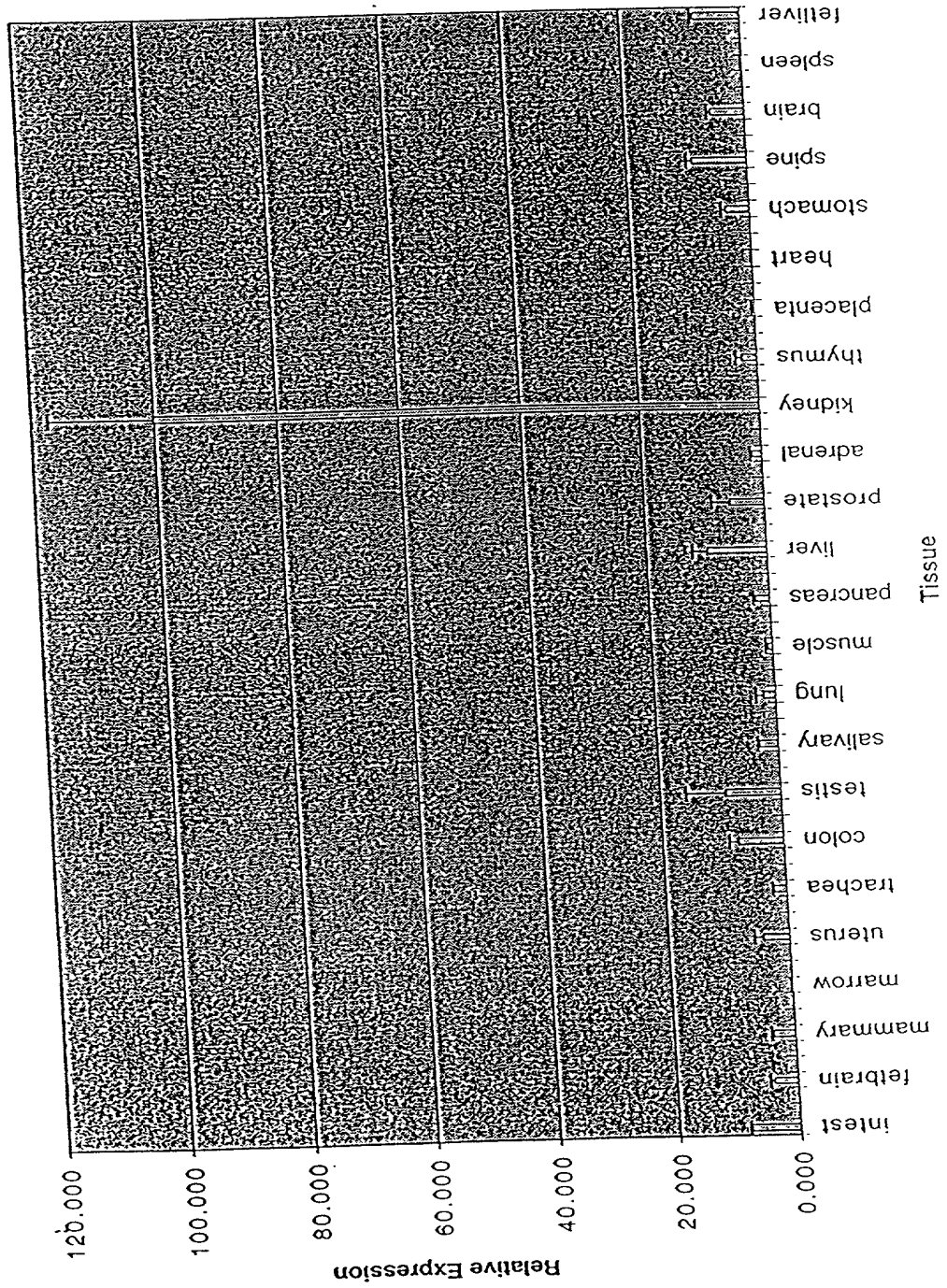
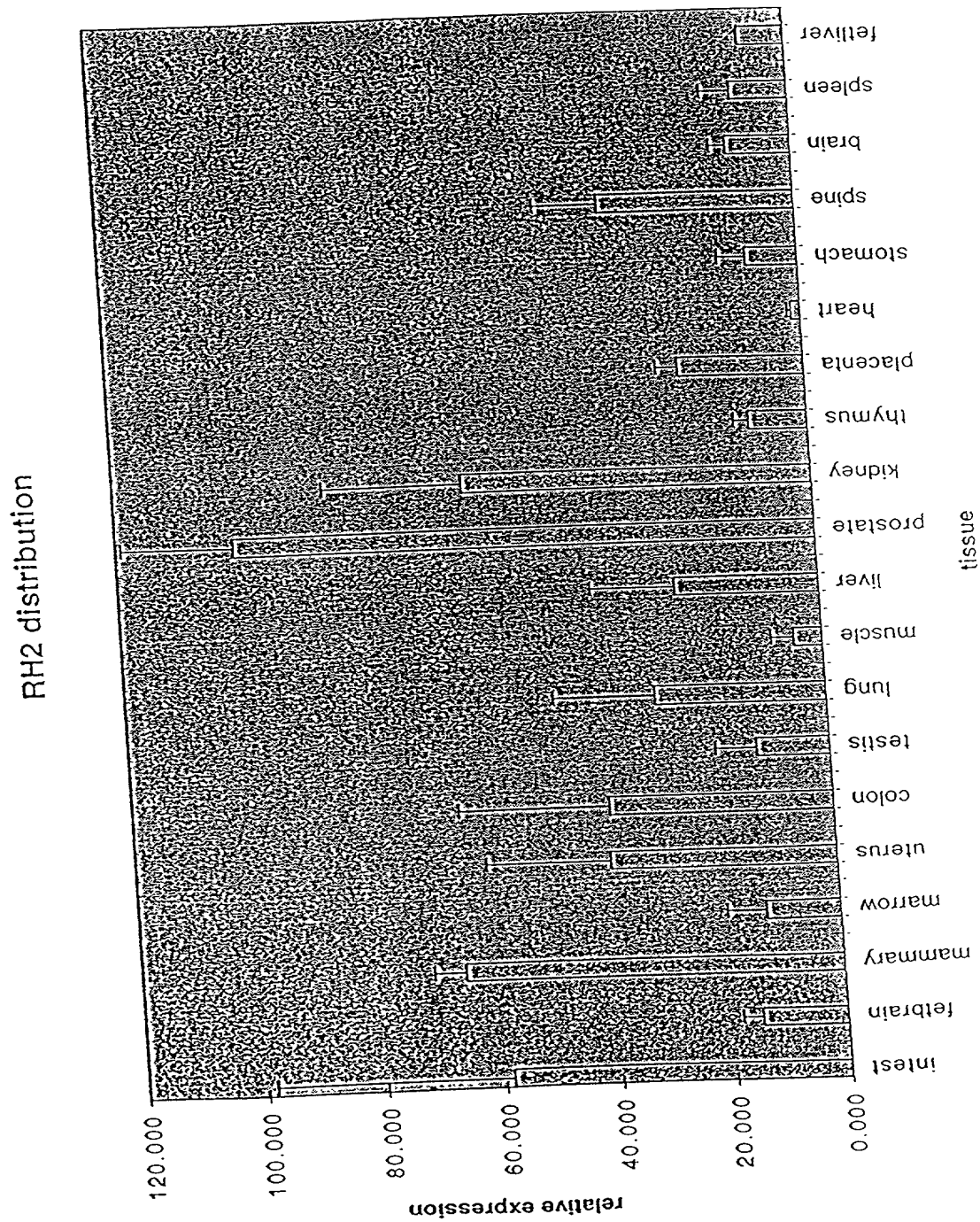


FIGURE 26



T0000T/510000T

FIGURE 27

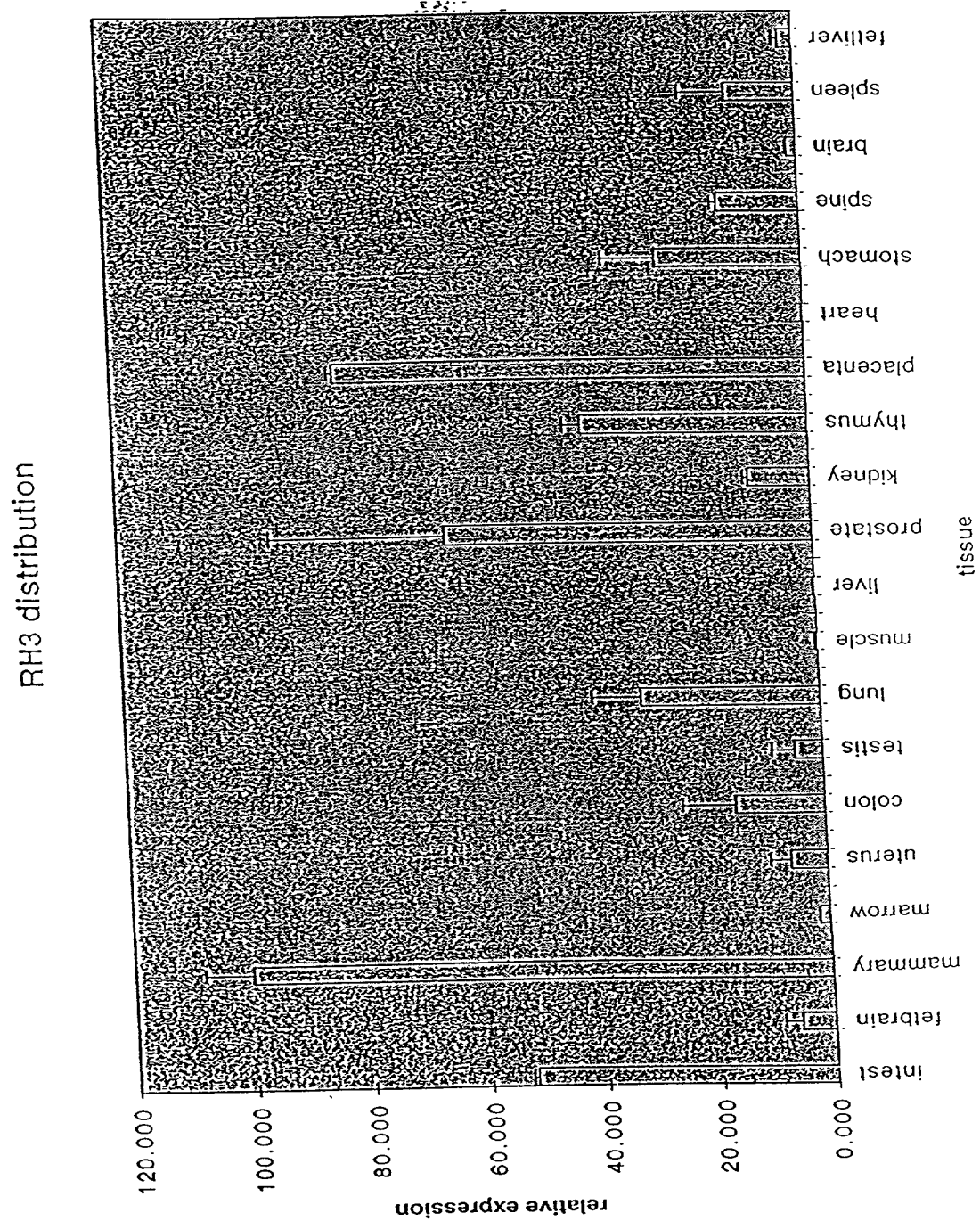


FIGURE 28

IL17 RH4 distribution

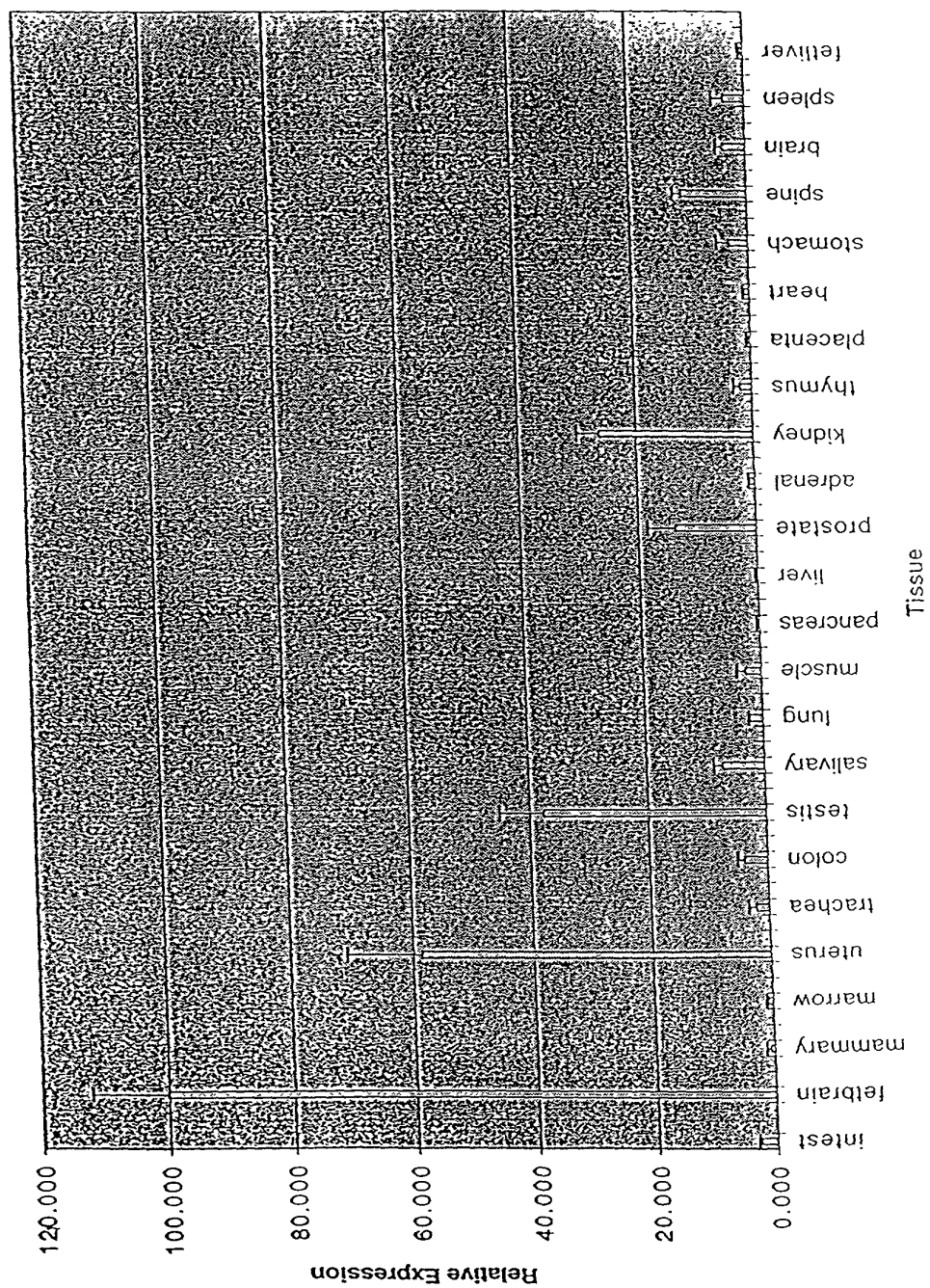
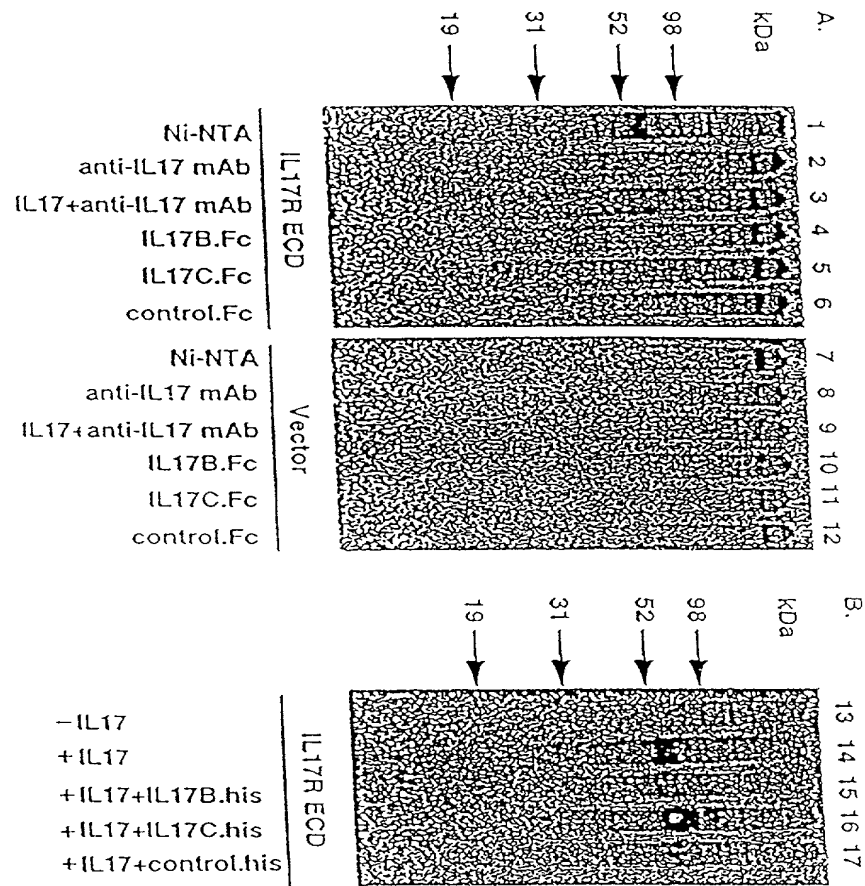


FIGURE 29



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FIGURE 30

h-IL17 1 - - - - - M T P G K T S L V S L L L L S L E A I V K A G I T I P R - - - - -

h-IL17B 1 - - - - M O W P H N L F L L T I S I F L G L G Q P R S P K S K R K G Q G R P G P - - - - -

h-IL17C 1 - - - - M I L L P G L L F L I W L H T C L A H H D P S L R G P H S H G T P H C Y S A E E L P L G

h-IL17E 1 M R E R P R L I G E D S S L I S L F L Q V V A F L A M V M G T H T Y S H W P S C C P - - - - -

h-IL17 30 - - - - - N P G C P N S E D K N F P R T V M V N L N I H N R N T N T N P K R - - - - -

h-IL17B 39 A P G P H Q V P L D L V S R M K P Y A R M E E Y E R N I E E M V A Q L R N S S E L A O R K C E V N

h-IL17C 47 A P P H L L A R G A K W G Q A L P V A L V S S L E A A S H R G R H E R P S A T T Q C P V L R P E E

h-IL17E 42 - - - - - S K G Q D T S E E L L A W S T V P V P P L E P A R P N R H P E S C R A S E

h-IL17 63 - S S D Y Y N R S T S P W N L H R N E D P E R Y P S V I W E A K C R H L G C I N A D G - - N V D Y

h-IL17B 69 Q L W M S N K R S L S P W G Y S I N H D P S R I P V D L P E A R C L C L G C V N P F T M Q E D R S

h-IL17C 97 L E A D T H O R S I S P W R Y R V D T D E D R Y P Q K L A F A E C L C R G C I D A R T G - R E T A

h-IL17E 79 - D G P L N S R A I S P W R Y E L D R D L N R L P Q D L Y H A R C L C P H C V S L Q T G S H M D P

h-IL17 110 M N S V P I Q Q E I L V L R R E - - - - - P P H C P N S F R L E K I L V S V G C T C V T P

h-IL17B 139 V S V P V F S Q V P V R R R L C P P P - - - - - P R T G P C R Q R A V M E T I A V G C T C I F -

h-IL17C 146 L N S V R L L Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V L P

h-IL17E 128 G N S E L L Y H N Q T V F Y R R P C H G E K - - - G T H K G Y C L E R R L Y R V S L A C V C V R P

h-IL17 151 V H H V A

h-IL17C 196 S V - - -

h-IL17E 175 V M G - -

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FIGURE 31A

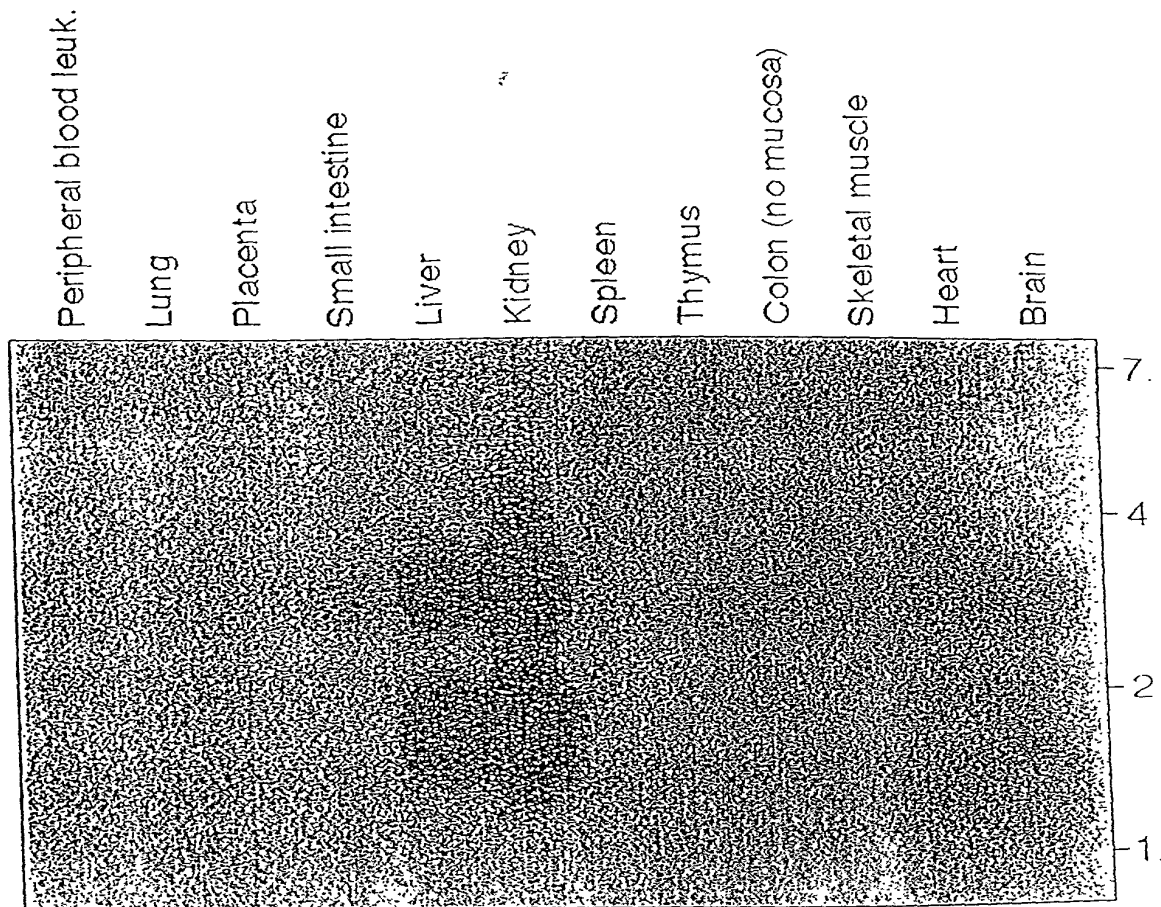


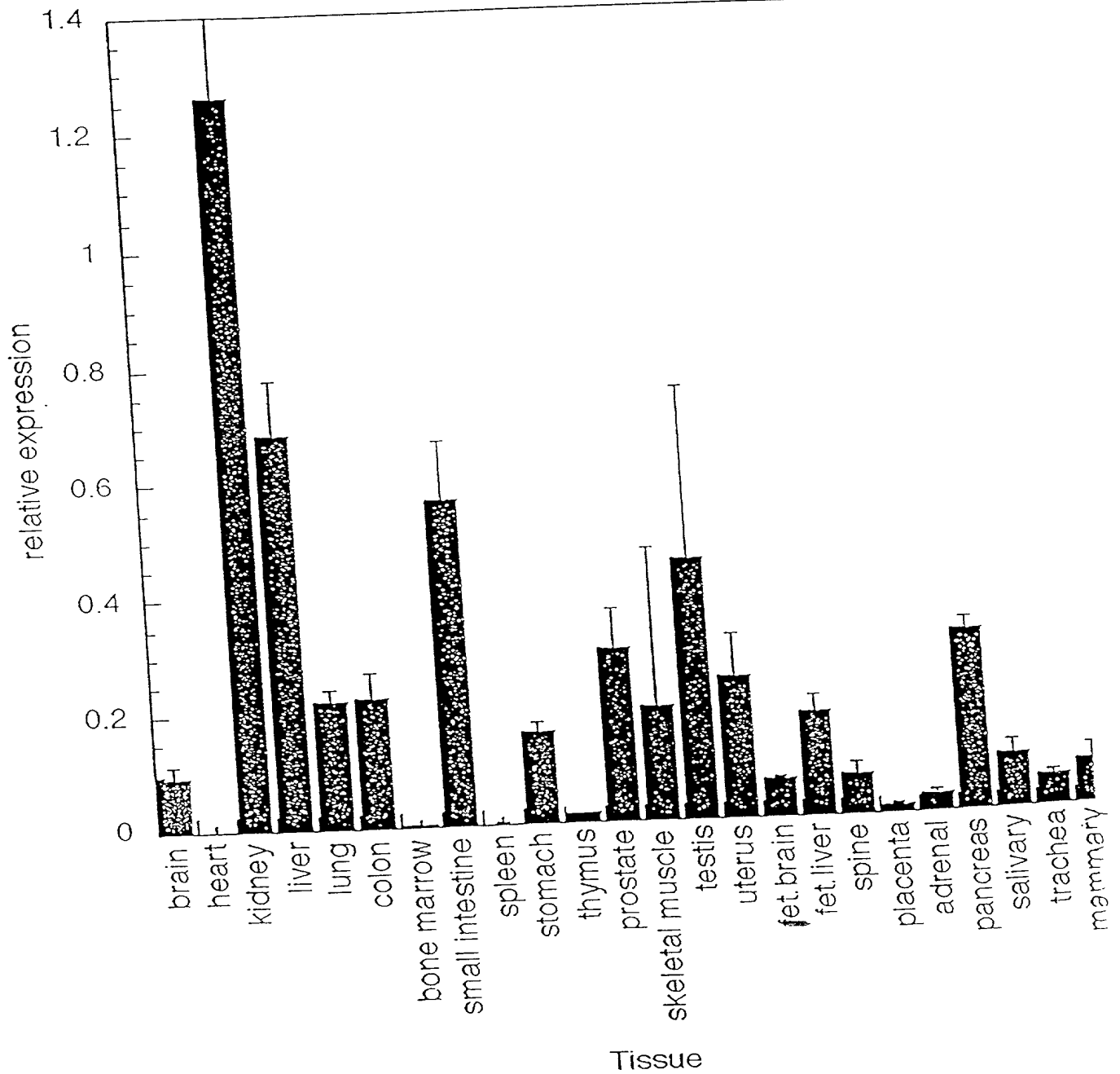
FIGURE 31B

FIGURE 32A

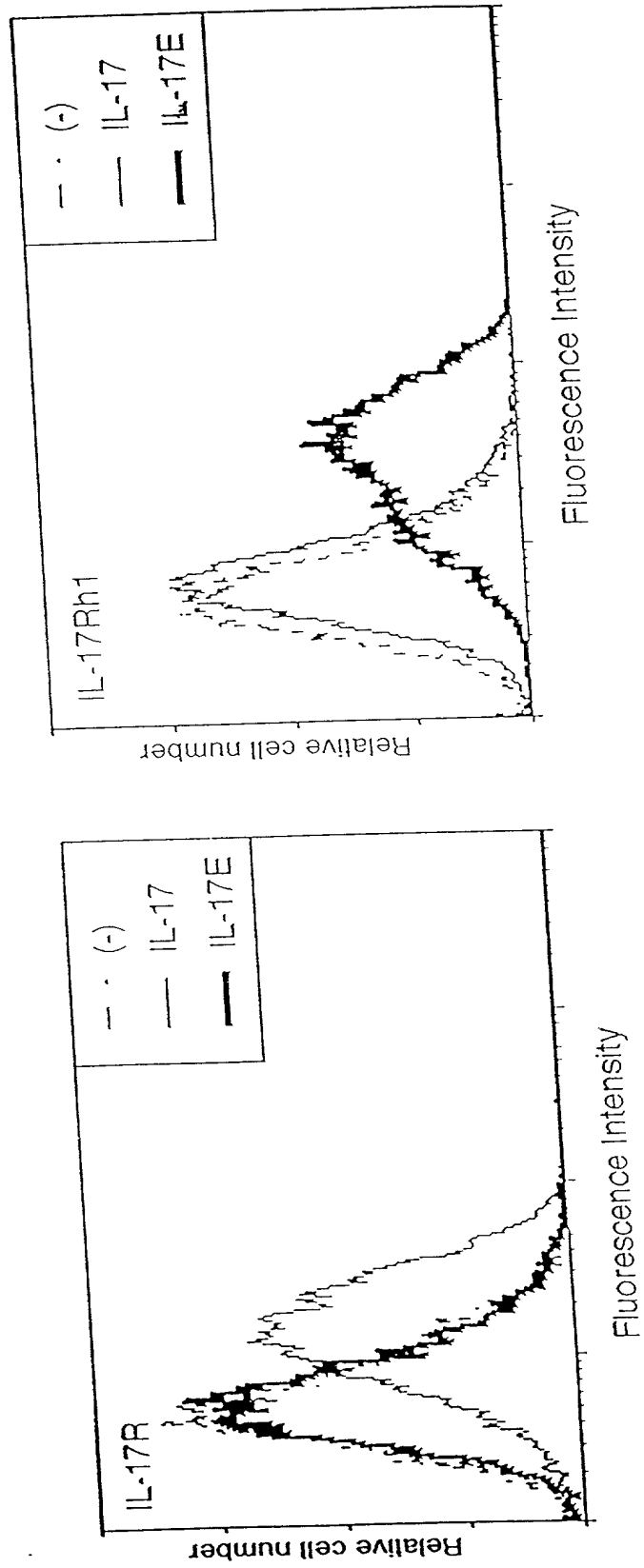
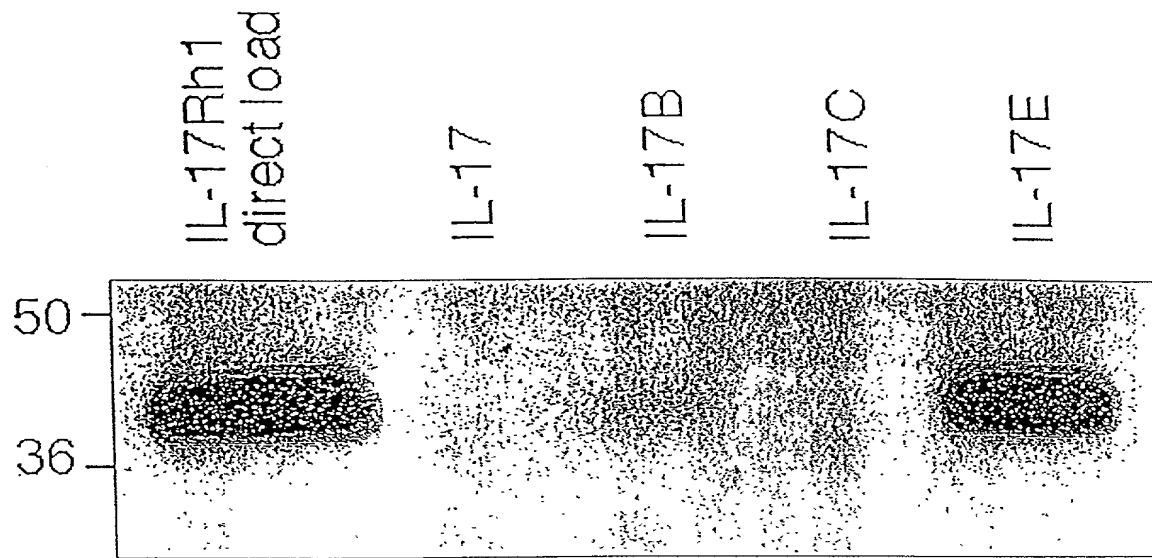


FIGURE 32B



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FIGURE 33

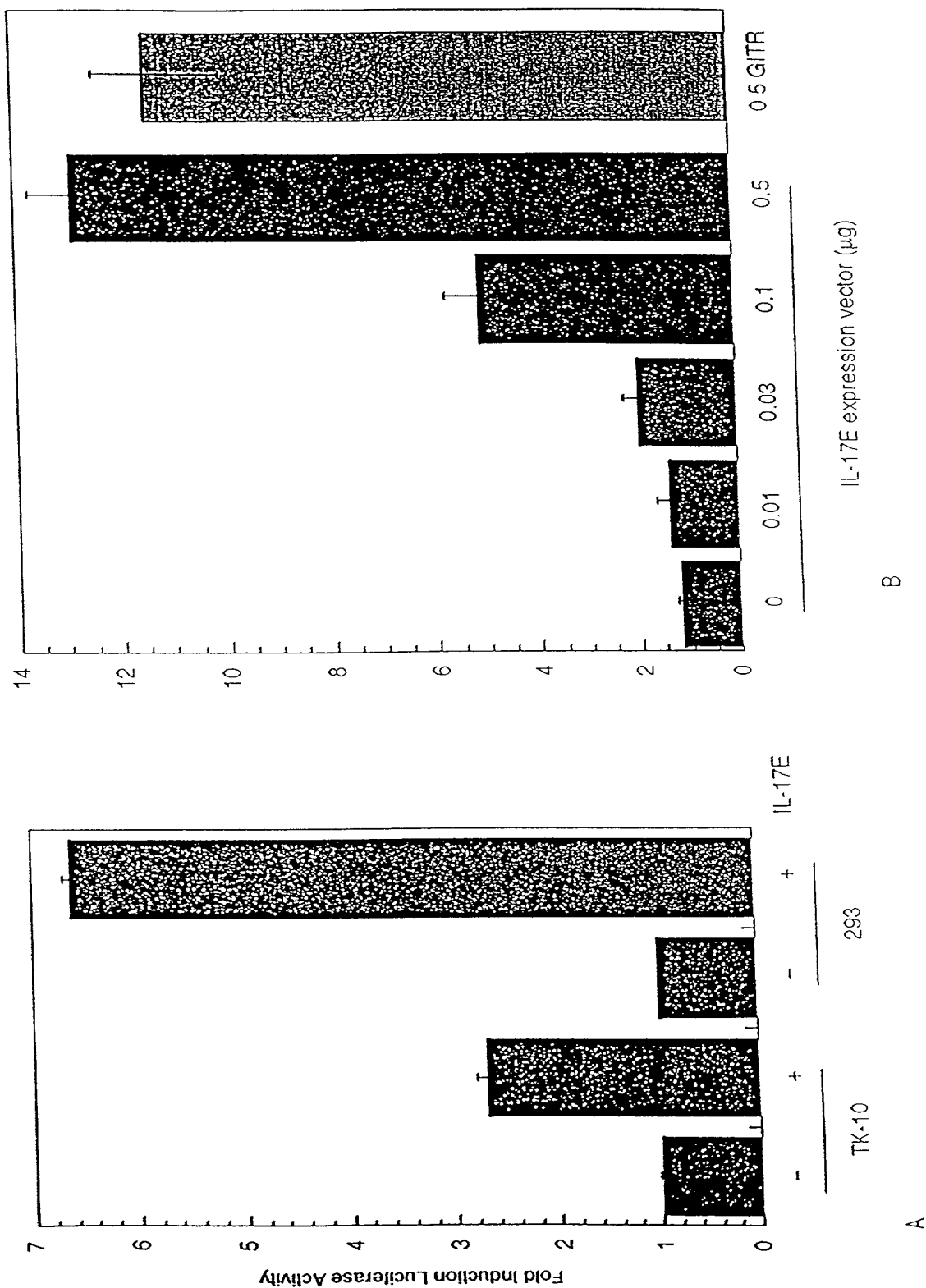
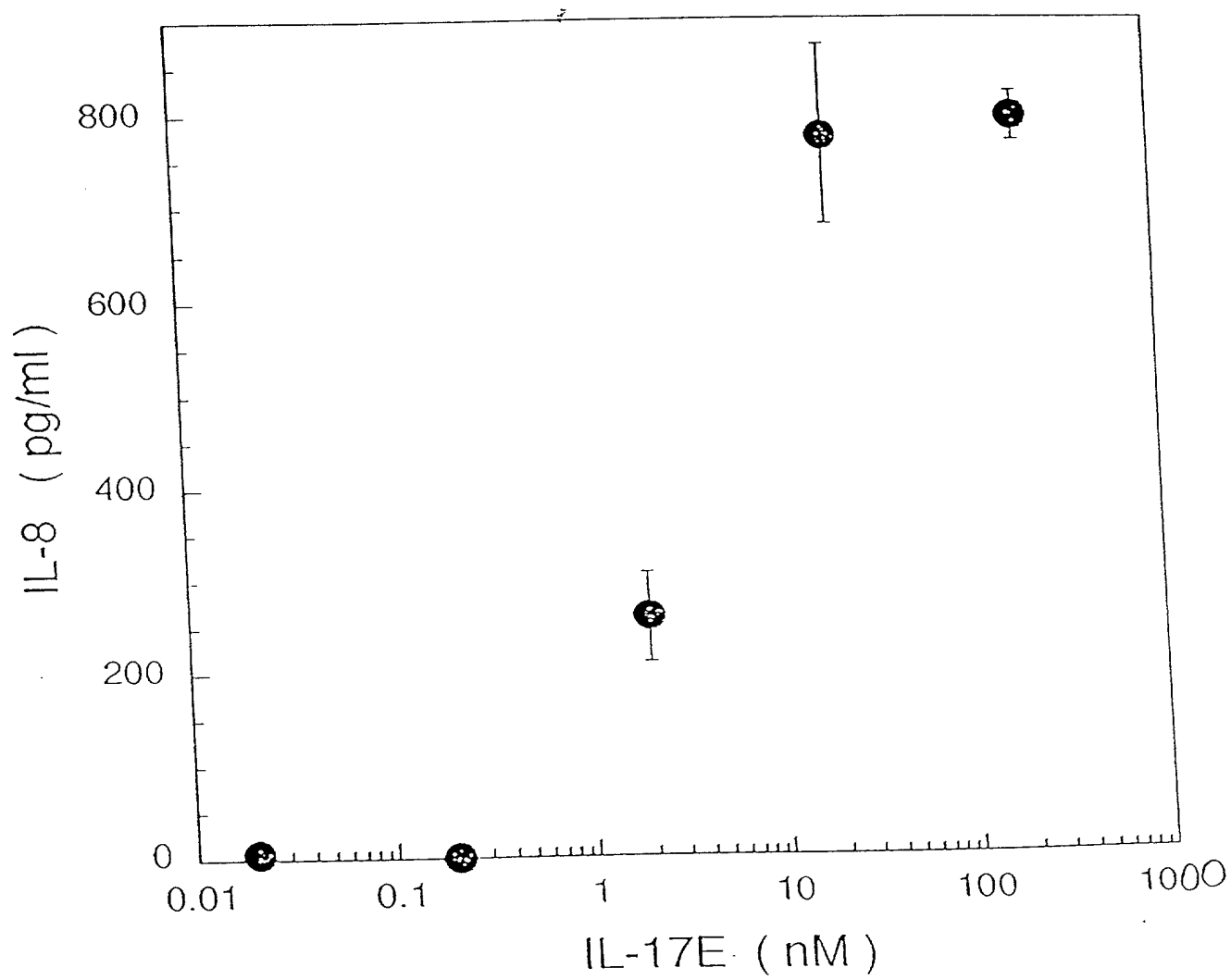


FIGURE 34

IL-17 family of cytokines has complex pattern
of overlapping receptor-ligand specificities

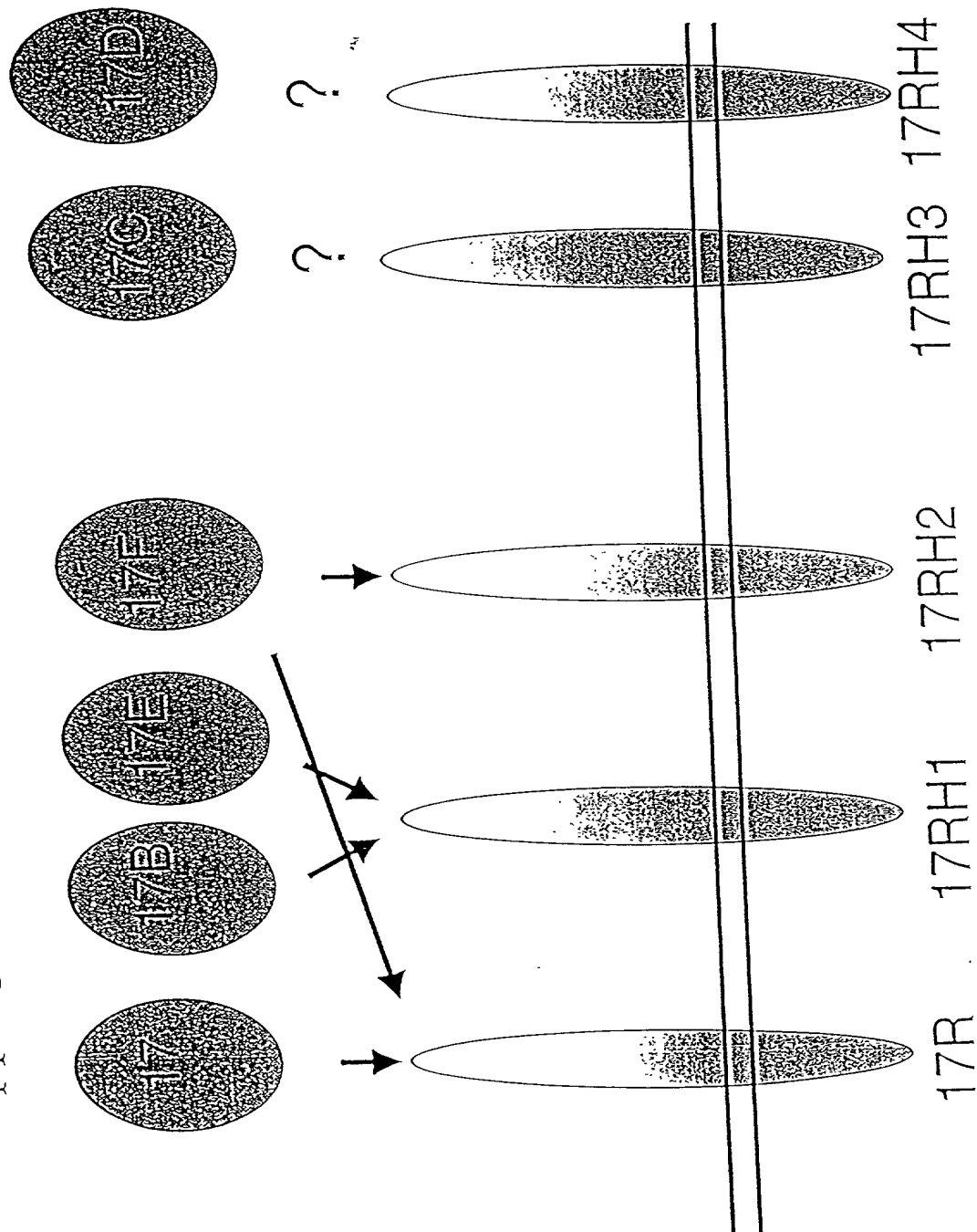


FIGURE 35

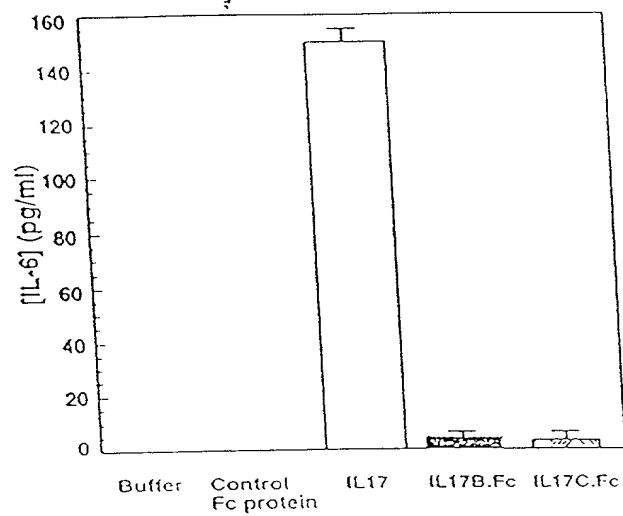
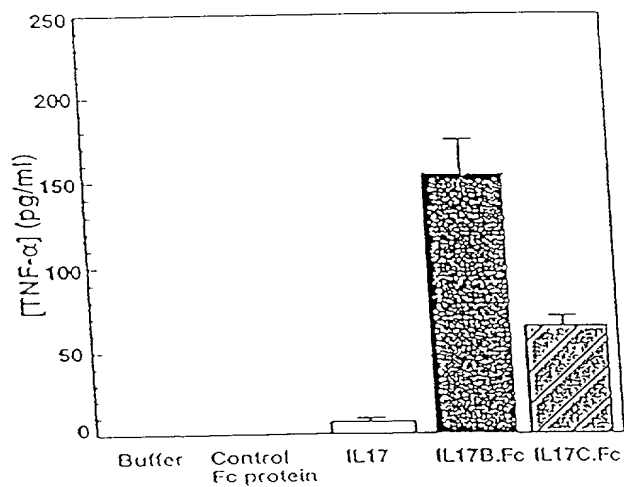
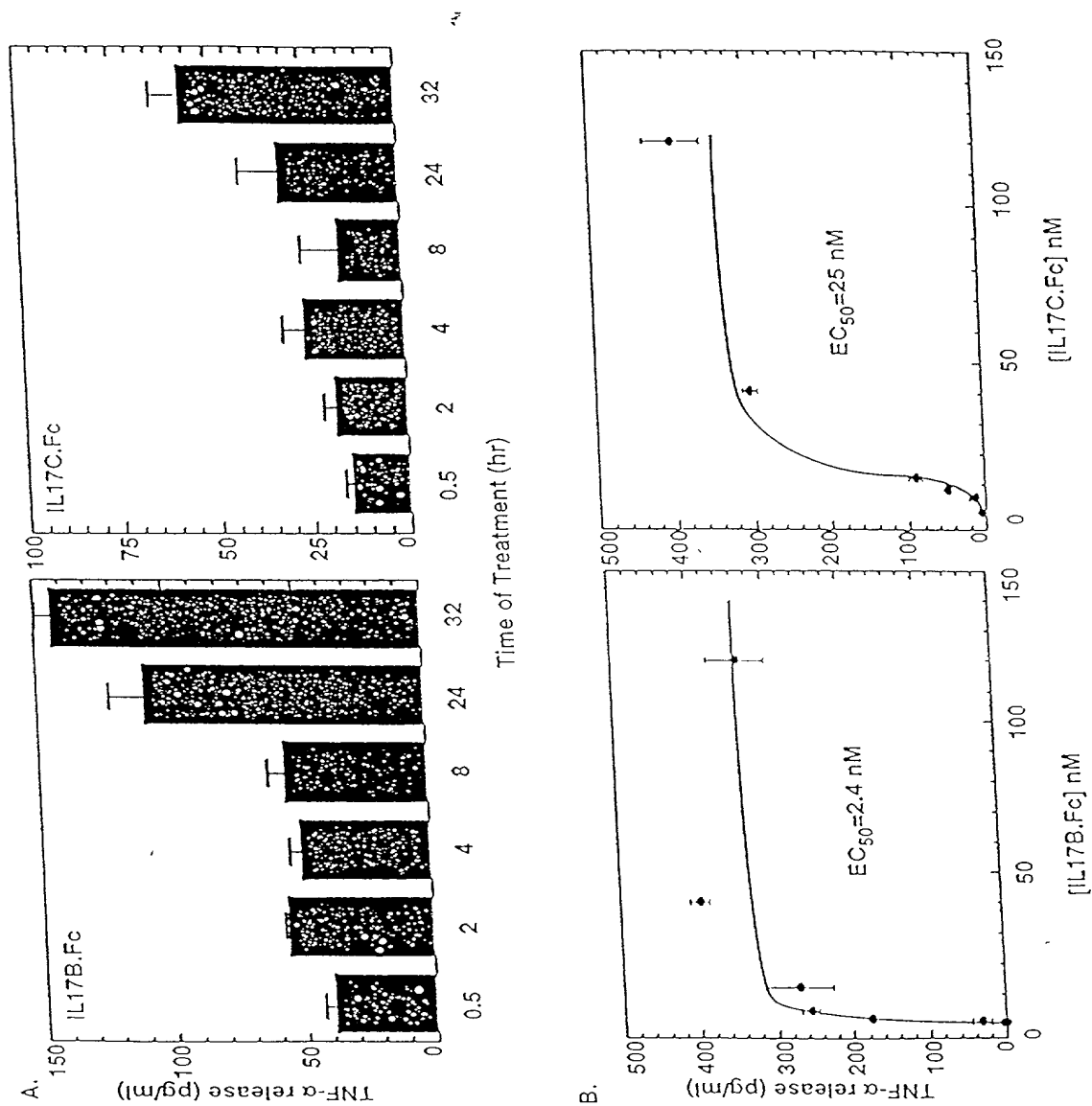
FIGURE 36**A. HFF cells****B. THP1 cells**

FIGURE 37



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FIGURE 38

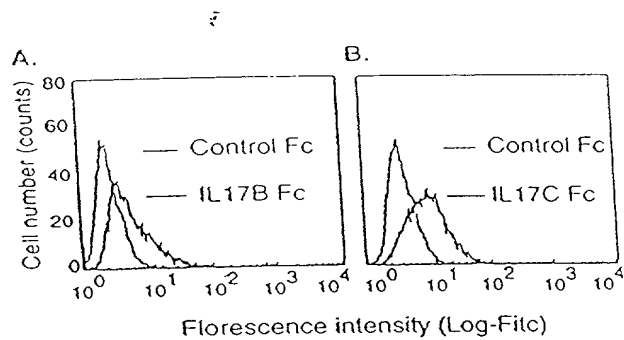


FIGURE 39

IL-17 induces breakdown and inhibits synthesis of cartilage matrix

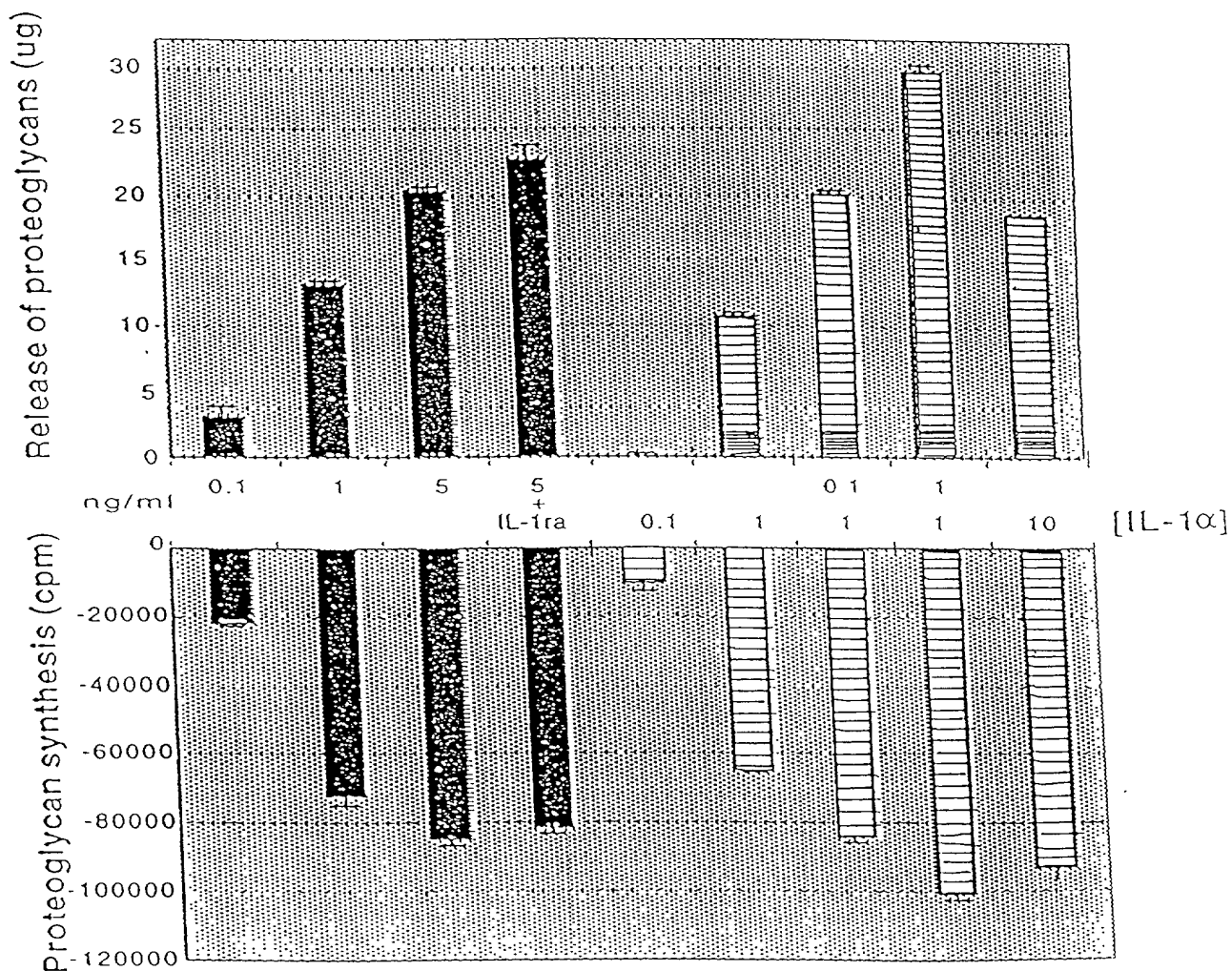


FIGURE 40

IL 17 increases basal and
IL-1 α -induced nitric oxide release

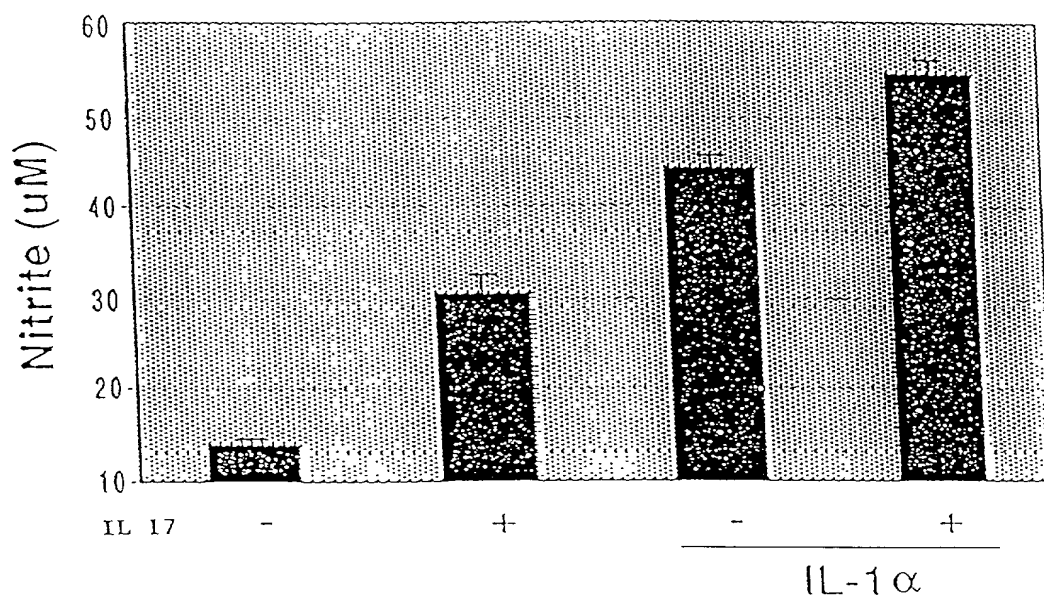
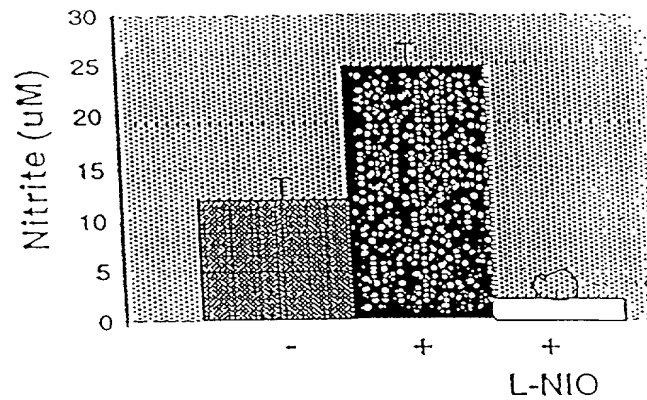


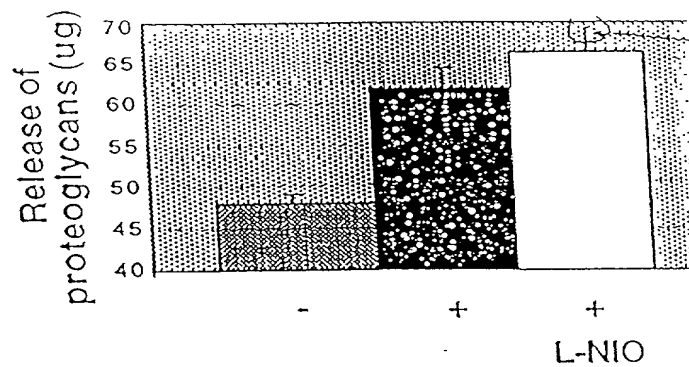
FIGURE 41

Inhibition of nitric oxide release does not block the detrimental effects of IL-17 on matrix breakdown or synthesis

A.



B.



C.

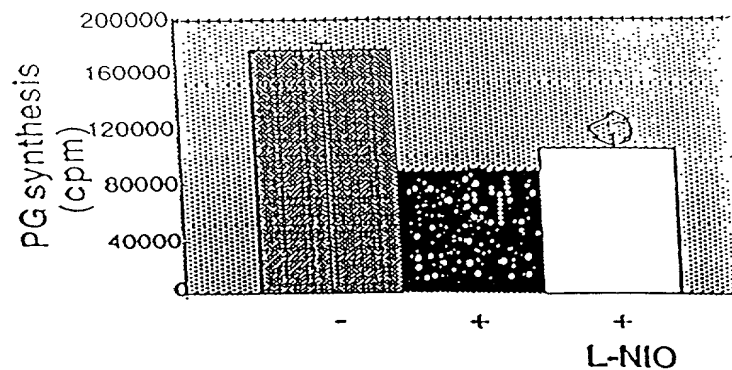
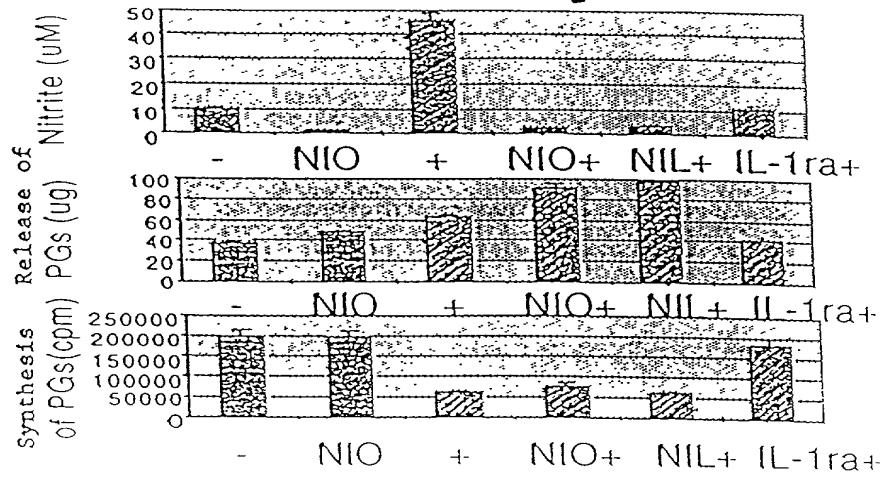


FIGURE 42

INHIBITION of NO release enhances
 IL-1- α -induced matrix breakdown
 but not matrix synthesis

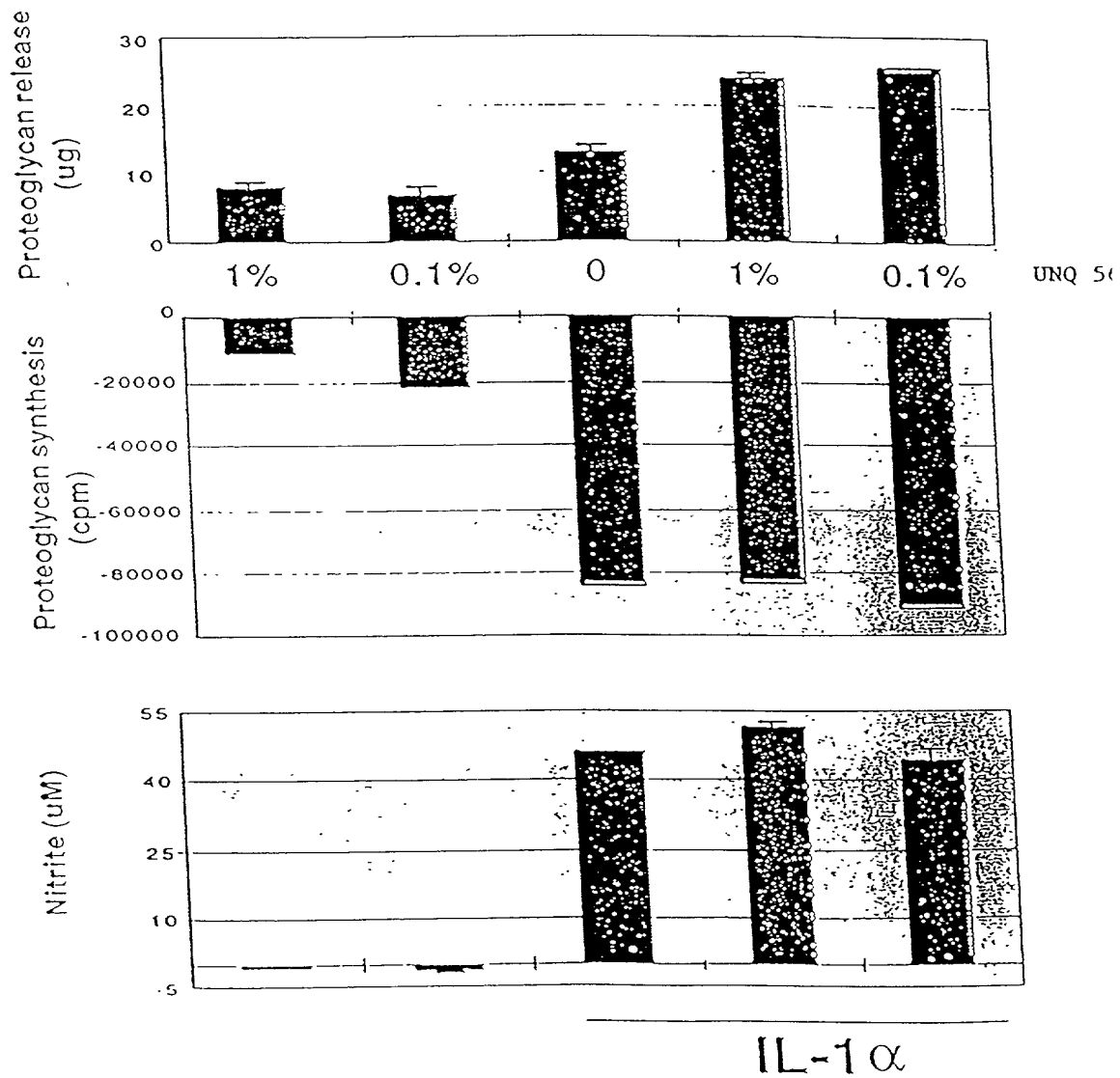


FOOTNOTES

FIGURE 43

IL-17C

detrimental effects on articular cartilage



Inflammatory Bowel Disease: Expression of IL-17 Family in Mouse Model of IBD

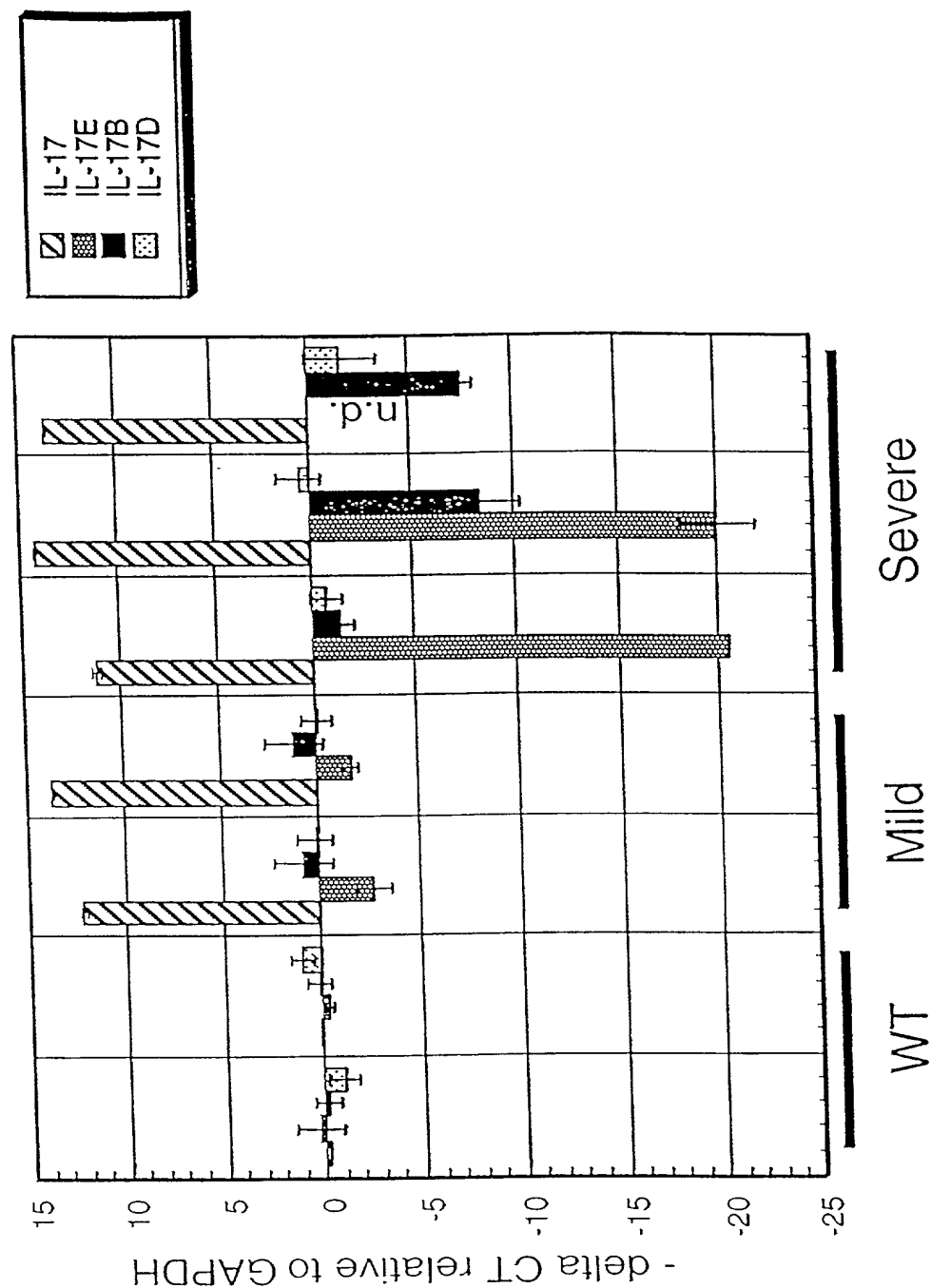


FIGURE 44

IL-17D, present in brain, decreases rapidly following stroke

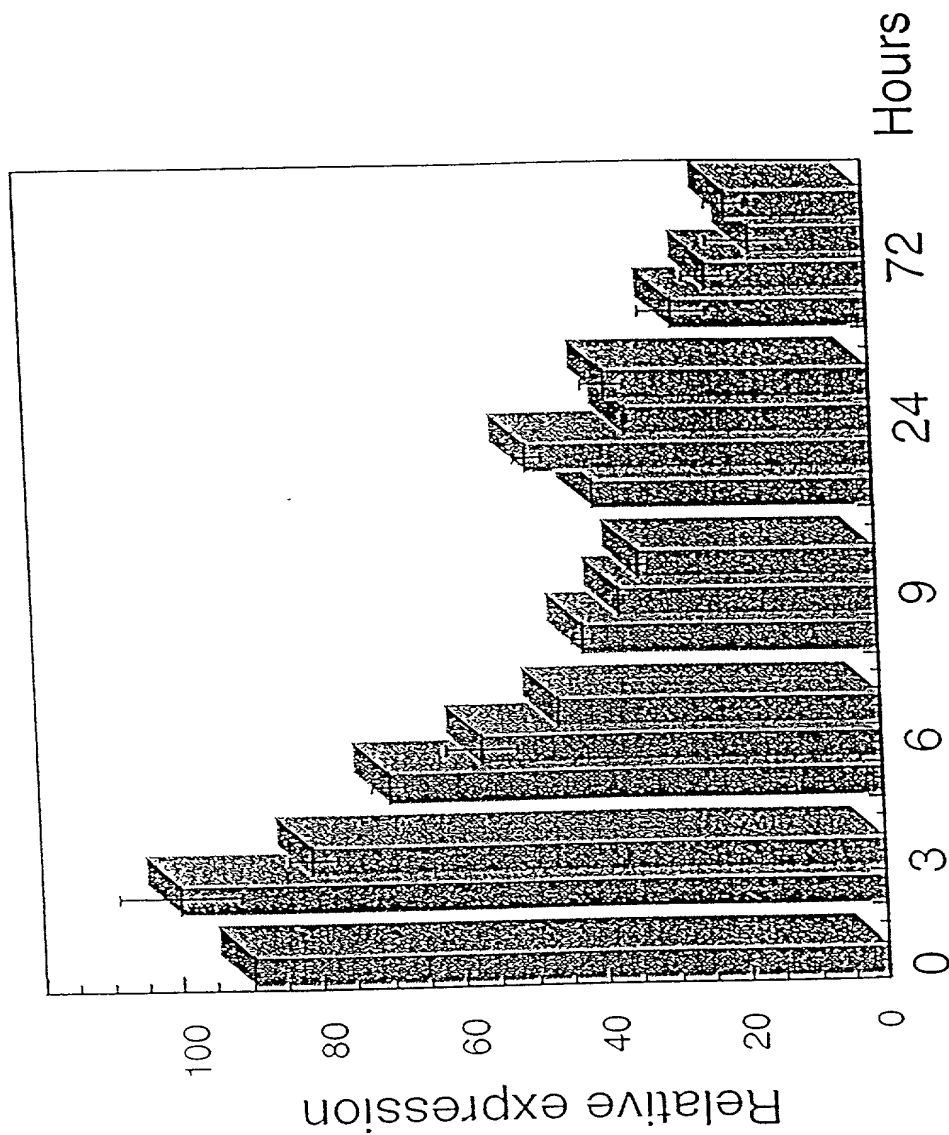


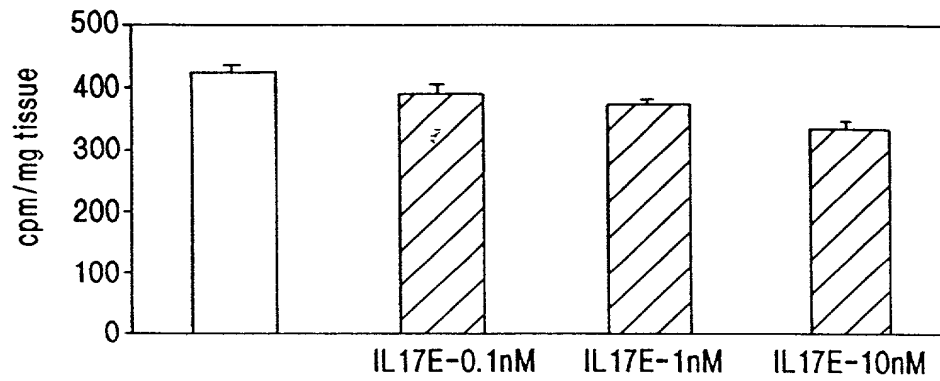
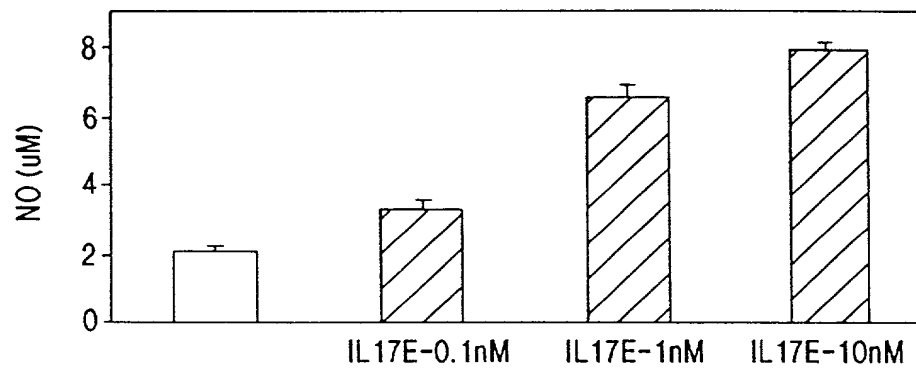
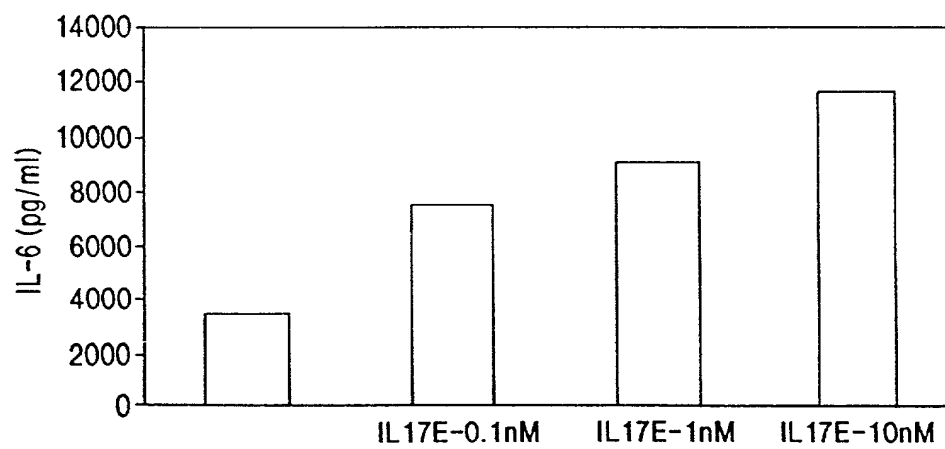
FIGURE 46**FIG. 46A****FIG. 46B****FIG. 46C**

FIGURE 47

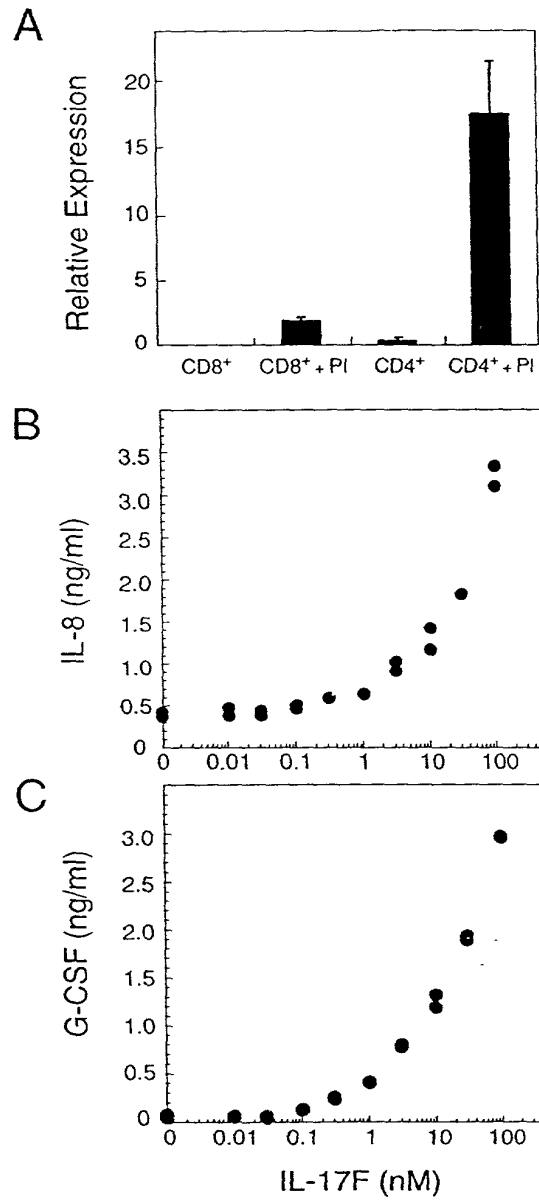


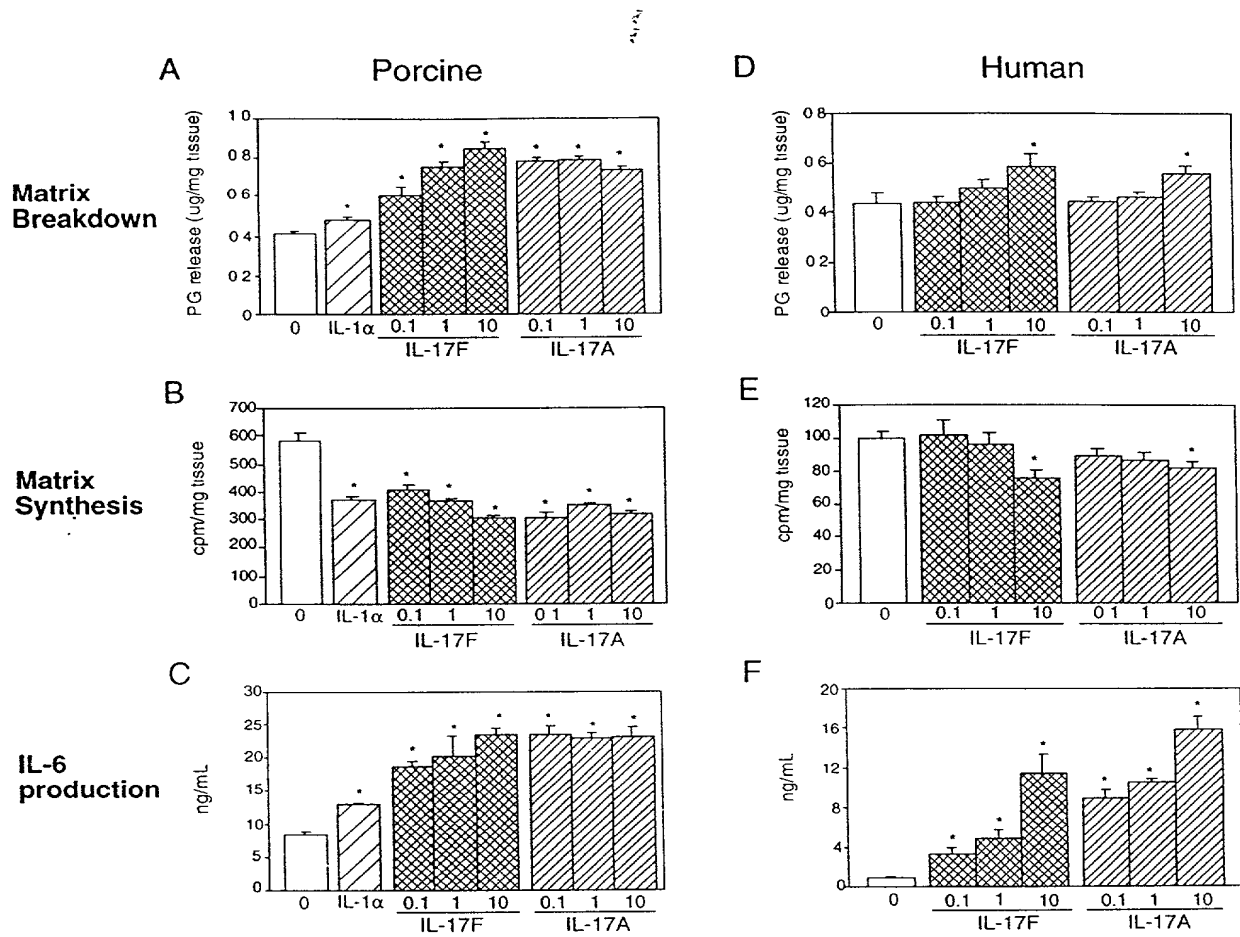
FIGURE 48

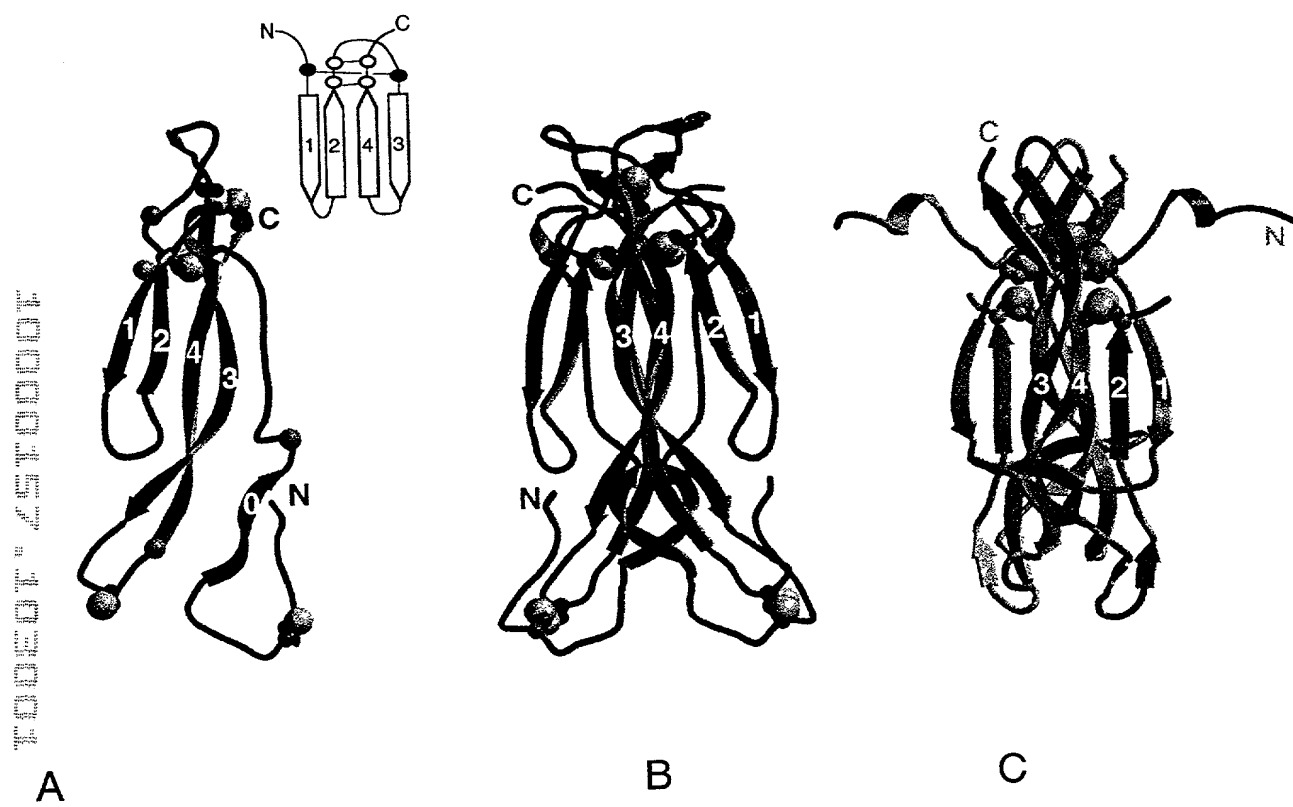
FIGURE 49

FIGURE 50

*

IL-17FRKIPKVG	HTFFQKPES	17
IL-17AIVKAG	ITIPRNP.G	14
IL-17BQPRS	PKSKRKGQGR	PGPLAPGPHQ	VPLDLVSRMK	PYARMEEYER	44
IL-17C	HHDPSLRGHP	HSHGTPHYS	AEELPLGQAP	PHLLARGAKW	GQALPVALVS	50
IL-17EYS	HWPS	PSKG	QDTSEELLRW	22

0

1

IL-17F	PPVPGG....SMKLDI	GIINENQRV	MSRNIESRST	PWNYTWTWD	59
IL-17A	PNSDKNFPR	TVMVNLNIHN	RNTNTN..PK	RSSDYNRST	PWNLHRNED	62
IL-17B	NIEEMVAQLR	..NSSELAQR	K.EV....NL	QLWMSNKRSL	PWGYSINHD	88
IL-17C	SLEAASHRGR	..HERPSATT	Q.PVLRPEEV	LEADTHQRSI	PWRYRVDTD	98
IL-17E	STVPVPPLP	..ARPNRHPE	S.RASE....	.DGPLNSRAI	PWRYELDRD	65

2

3

IL-17F	PNRYPSEVVQ	AQ RNLG IN	A..QKEDIS	MN VPI.QQE	TLVVRRKHQ	106
IL-17A	PERYPSEVIWE	AK RHLG IN	A..DGNVDYH	MN VPI.QQE	ILVLRREPPH	109
IL-17B	PSRIPVDLPE	AR L LG VN	PF.TMQEDRS	MV VPV.FSQ	VPVRRR...L	133
IL-17C	EDRYPQKLAF	AE L RG ID	AR.TGRETAA	LN VRL.LQS	LLVLR...RP	144
IL-17E	LNRLPDLYH	AR L PH VS	LQTGSHMDPR	GN ELLYHNQ	TVFYRRP...	112

4

*

IL-17F	SV.....SFQLEK	VL..VTVG T	VTPVIHHVQ	...	133
IL-17A	PN.....SFRLEK	IL..VSVG T	VTPIVHHVA	...	136
IL-17B	PPPPRTGP.RQRA	VMETIAVG T	IF.....	...	160
IL-17C	SRDGSGGLPT	PGAFAFHTEF	IH..VPVG T	V.LPRSVAA	ALE	184
IL-17E	HGEKGTHKGY LER	RLYRVSLA V	VRPRVMG..	...	145

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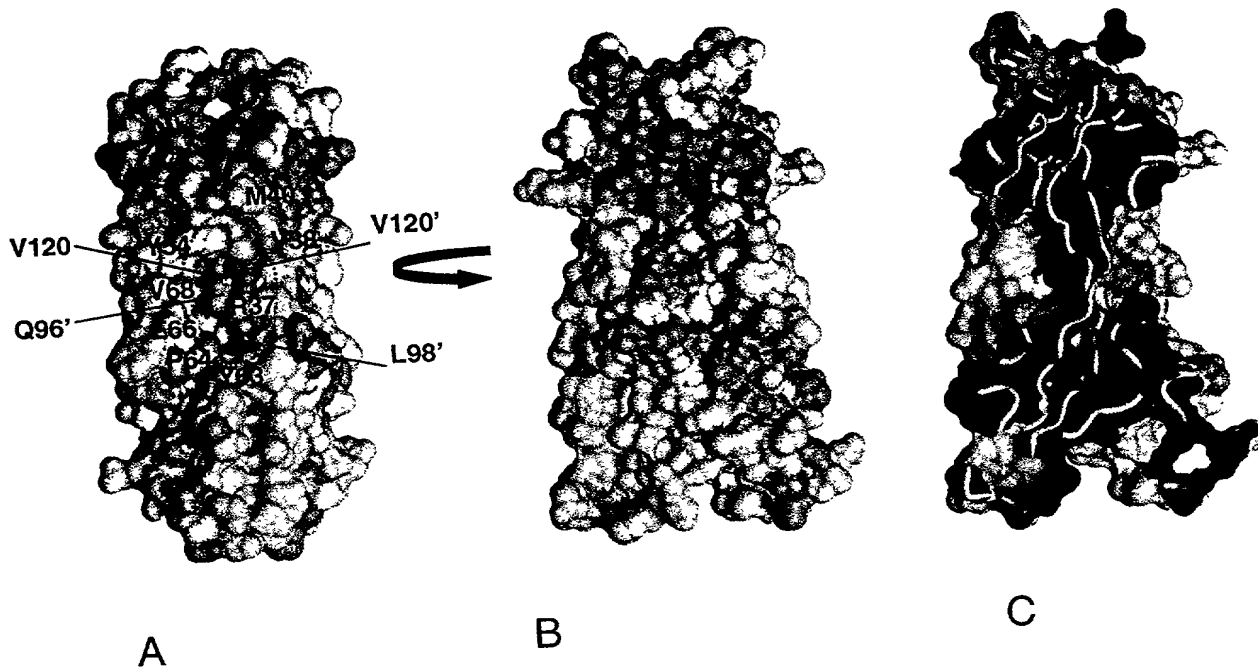
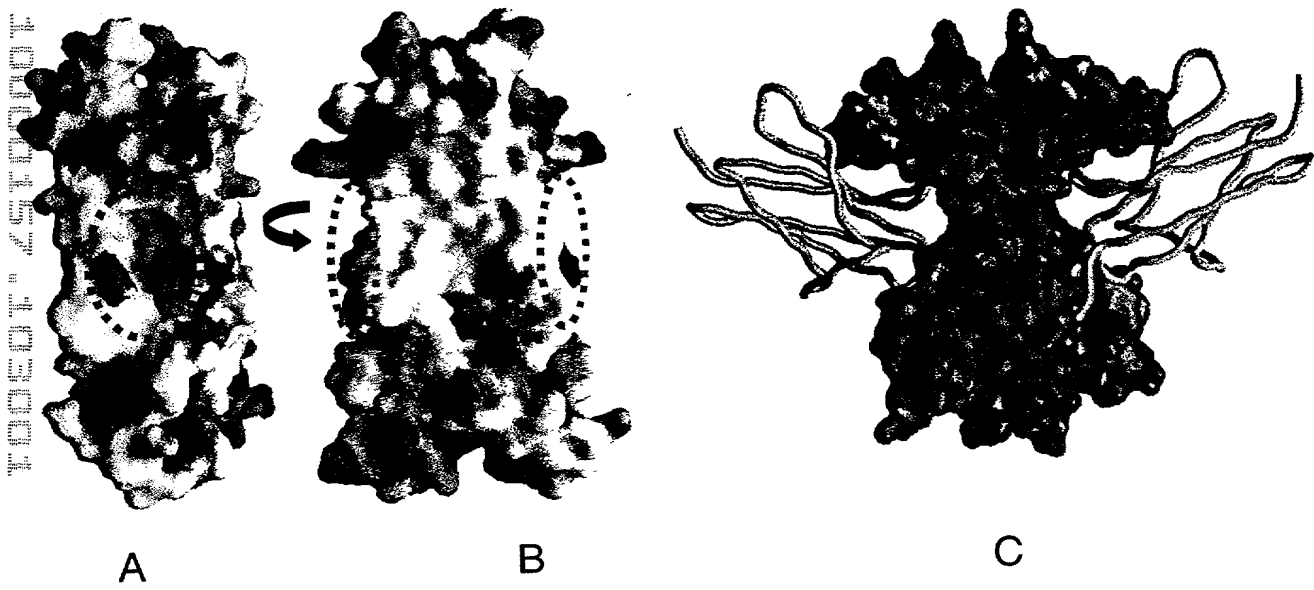
FIGURE 51

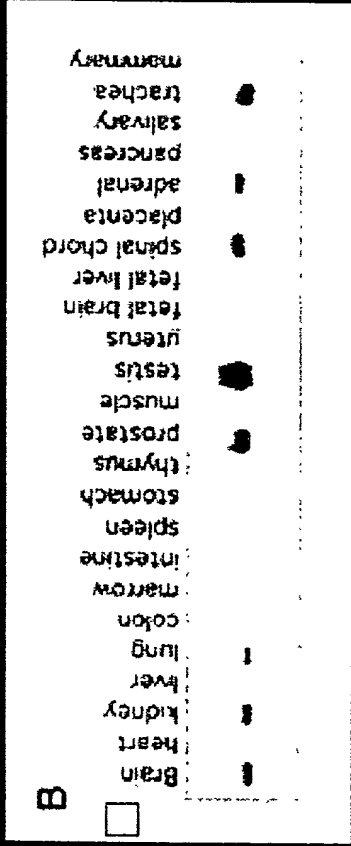
FIGURE 52



Variable	Mean	SD	Min	Max
Age	31.1	4.2	20	45
Gender	0.5	0.5	0	1
Marital status	0.4	0.5	0	1
Education	12.5	1.5	10	15
Income	1.2	0.8	0.5	2.5
Health status	0.3	0.4	0	1
Stress level	2.1	1.2	1	4
Life satisfaction	3.5	1.0	2	5
Work-life balance	2.8	1.1	1	4
Family support	0.6	0.5	0	1
Community support	0.4	0.5	0	1
Healthcare access	0.7	0.6	0	1
Quality of life	3.2	1.2	2	5
Overall well-being	3.8	1.1	2	5

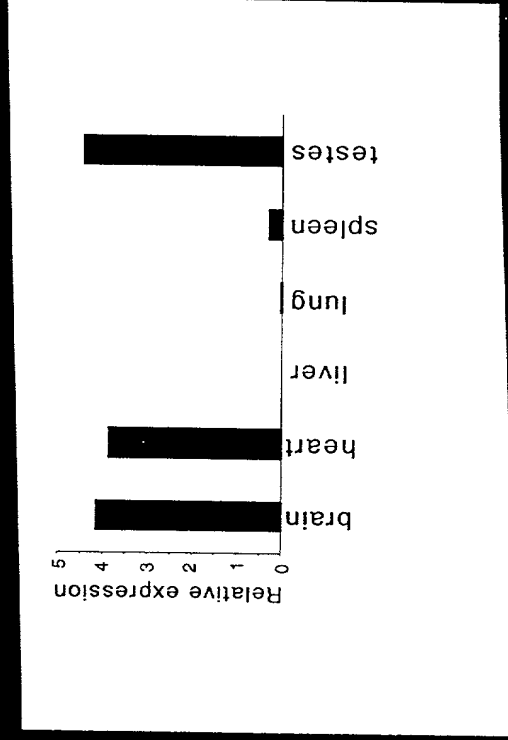
[illegible]

Tissue distribution of IL-17E



Human

IL-17E (PCR then probed with cDNA)



Mouse

Taqman assay

FIGURE 54

mL-17E transgenics are growth retarded

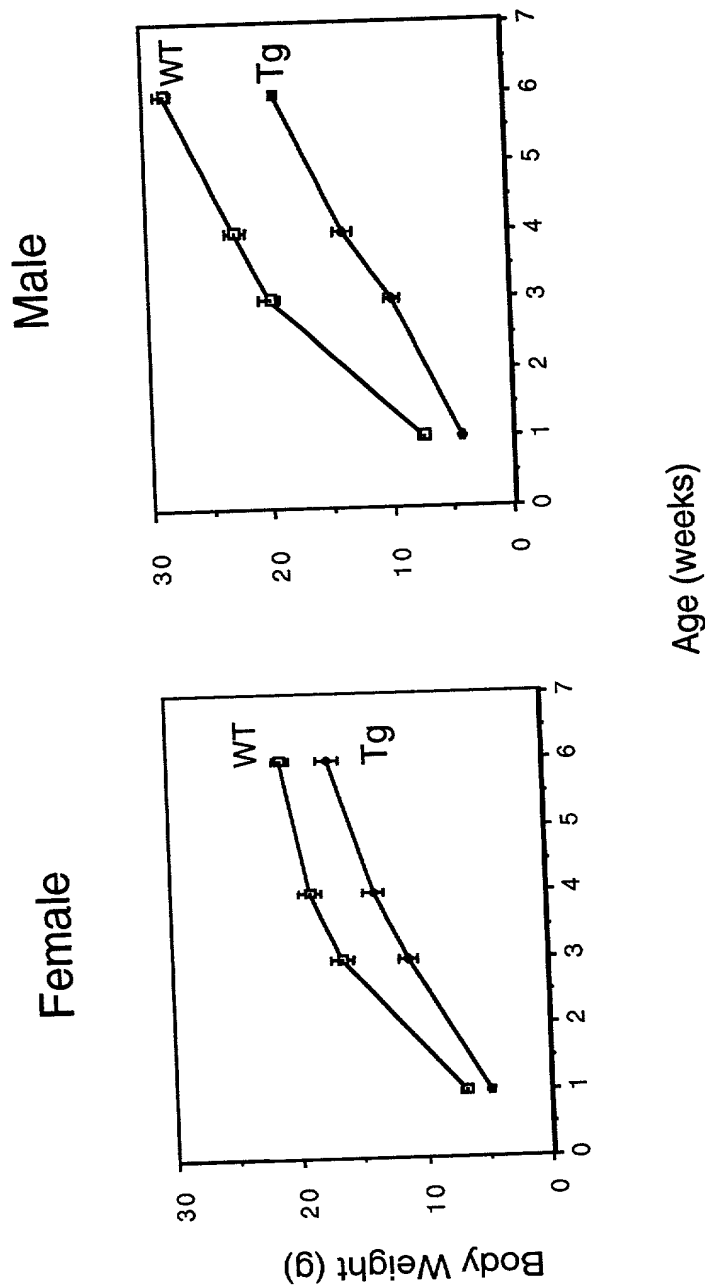


FIGURE 55

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IL17E transgenics are jaundiced by 6 weeks of age

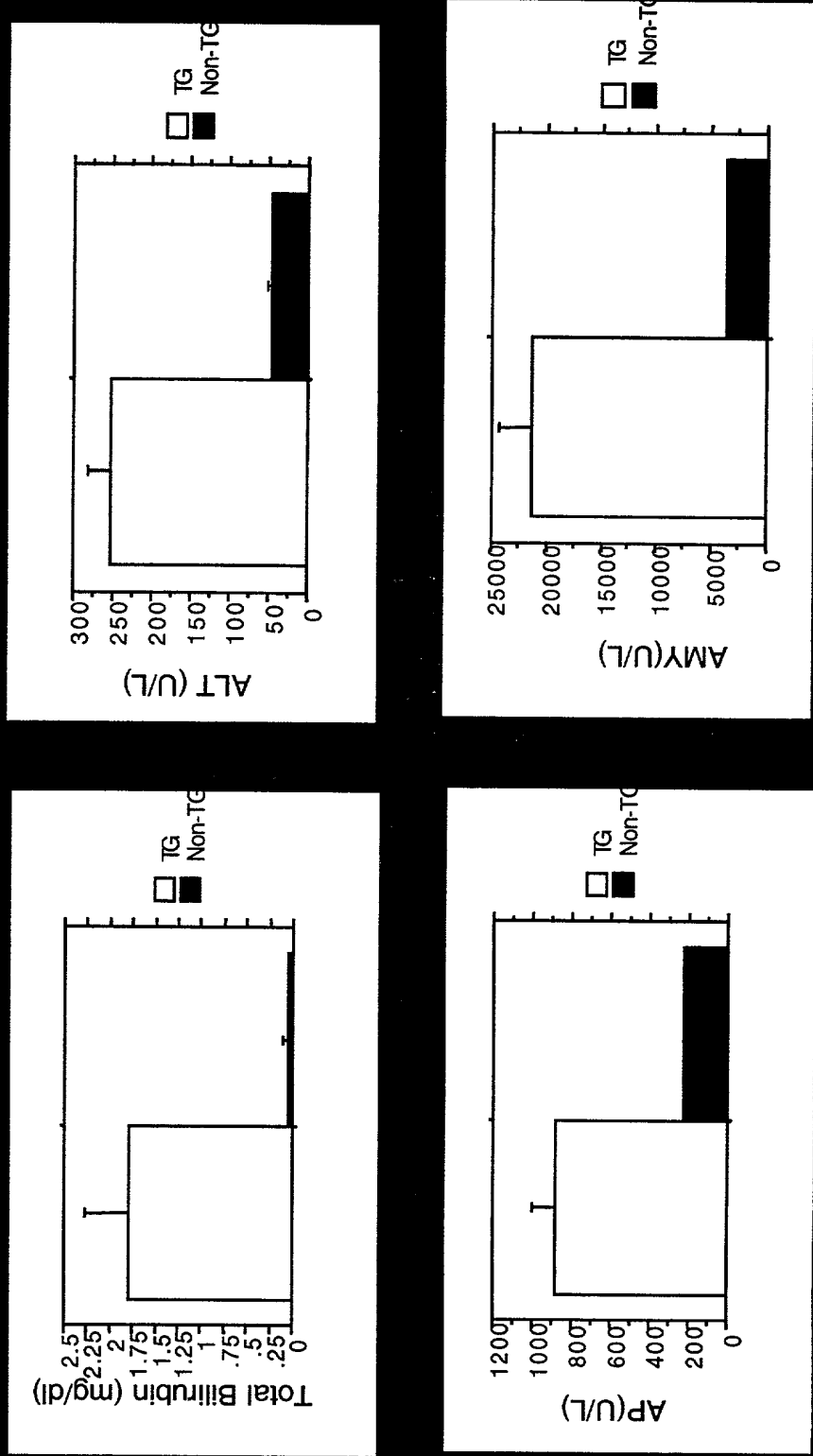


FIGURE 56

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FIGURE 57

mL-17E transgenics have elevated
total bilirubin and liver enzymes



Gene	Relative expression (TG vs Non-TG)
IL-1	~10
IL-4	~800
IL-5	~10
IL-10	~10
IL-12	~10
IFN γ	~10
TNF α	~10
GRO α	~10
MCP1	~10
G-CSF	~10
ICAM1	~50

FIGURES 58B - 58C

Relative expression
(TG vs Non-TG)

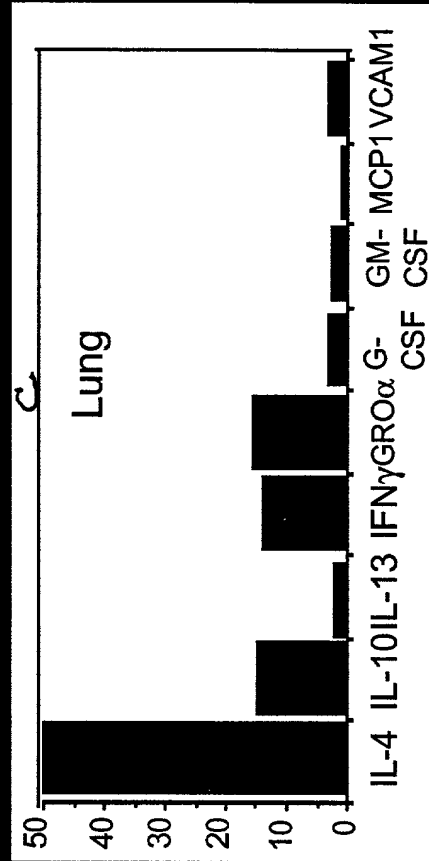
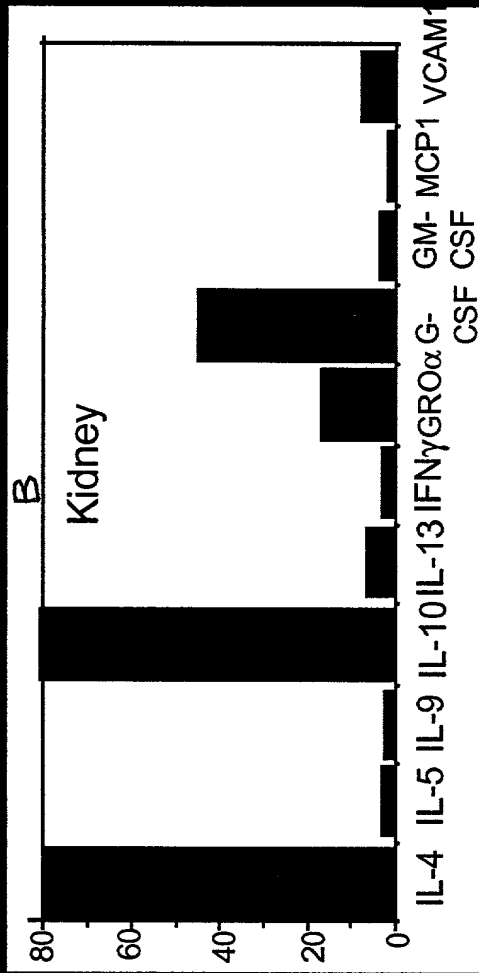




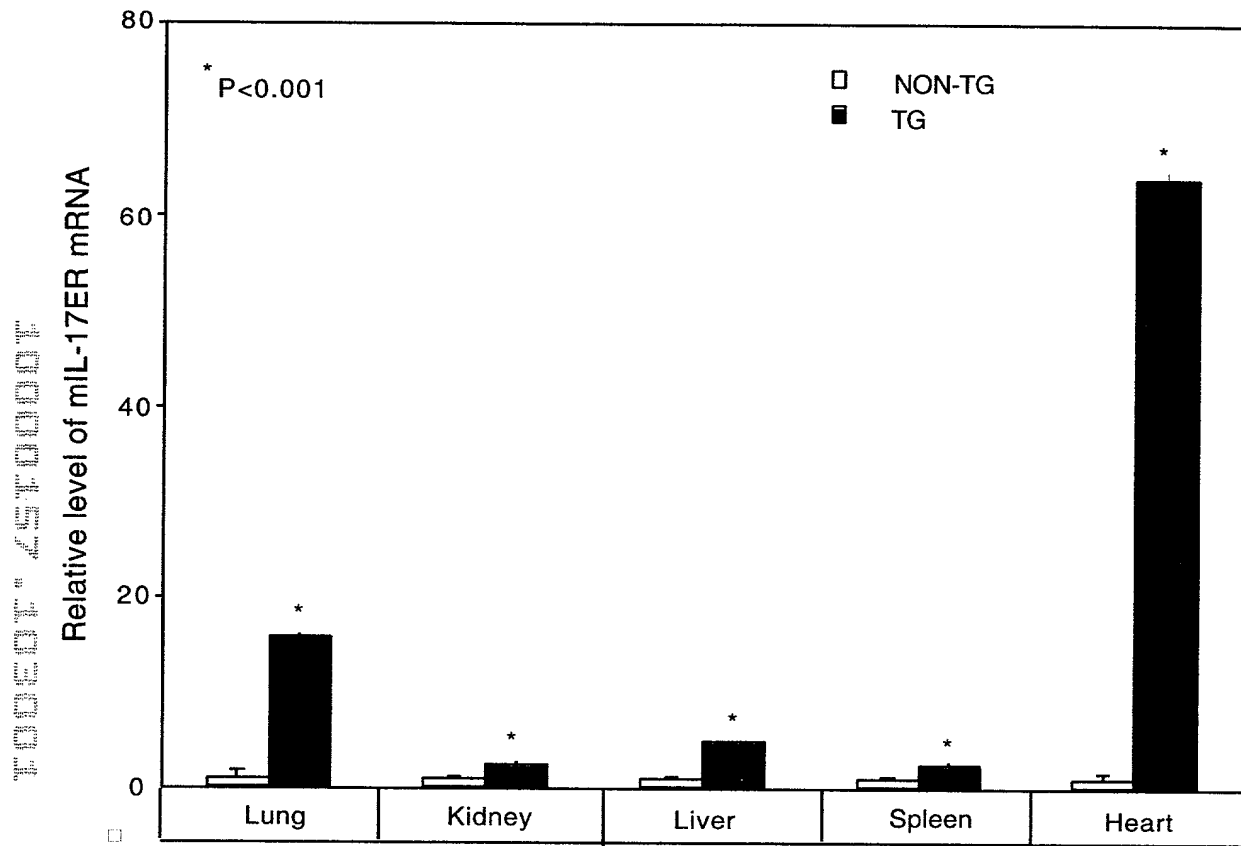
FIGURE 59

FIGURE 60

Elevated serum IL-5, IL-13 and TNF α
in mIL-17E transgenics

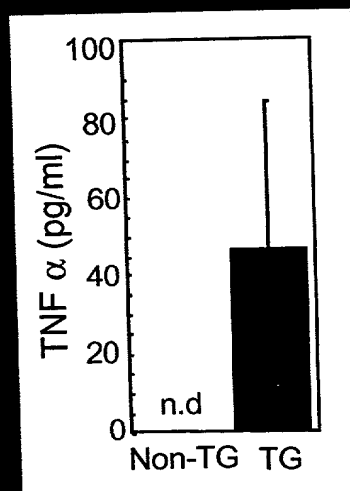
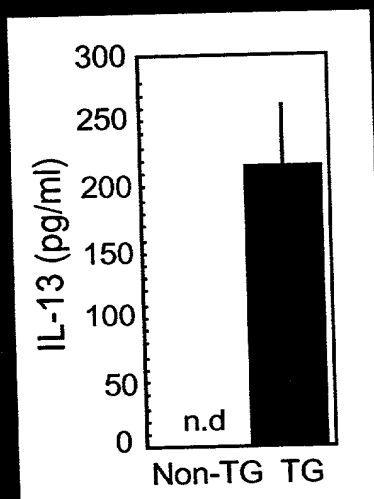
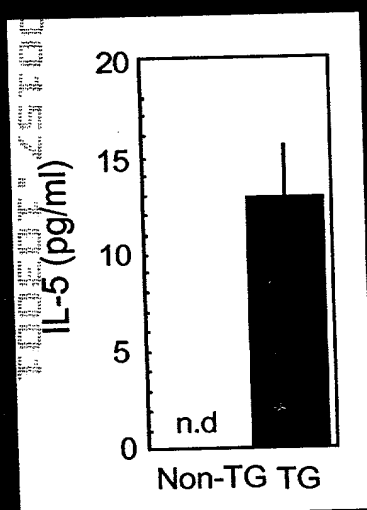


FIGURE 61

Serum IgE and IgG1, but not IgG2a is elevated in mIL-17E transgenics

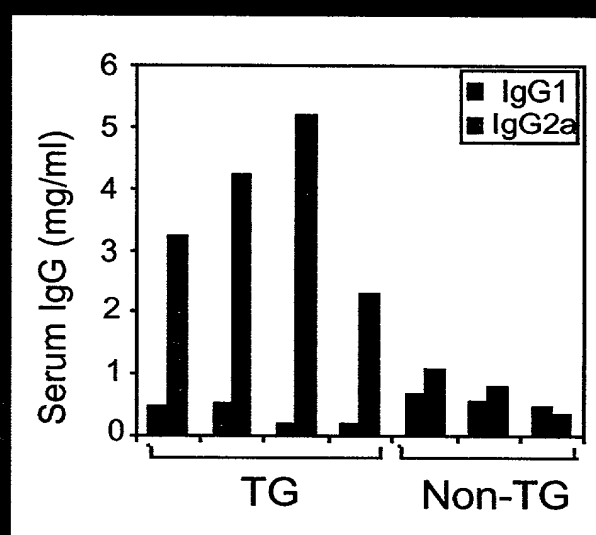
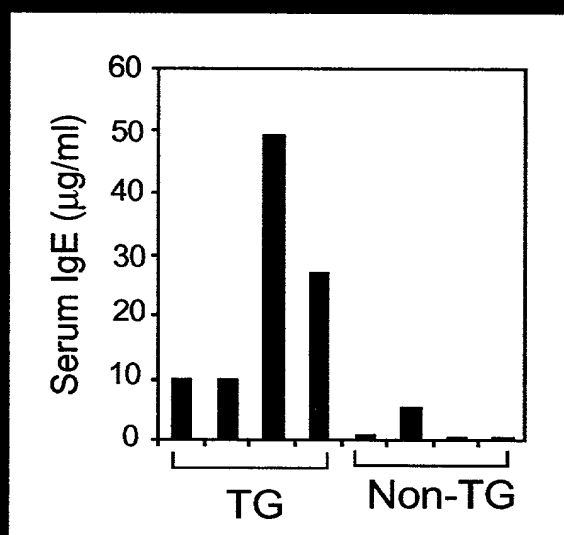


FIGURE 62

Neutrophilia in mIL-17E transgenics (8 wks, PBMC by FACS)

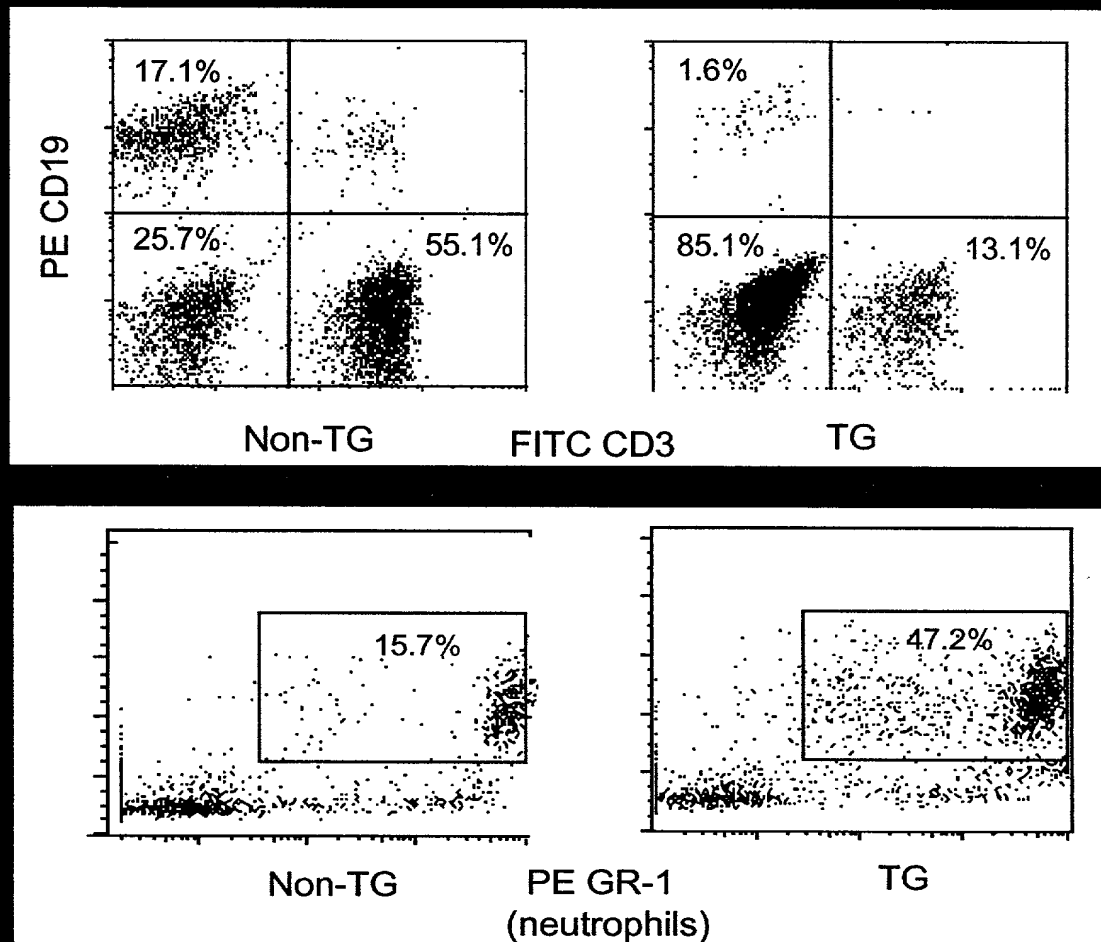


FIGURE 63

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

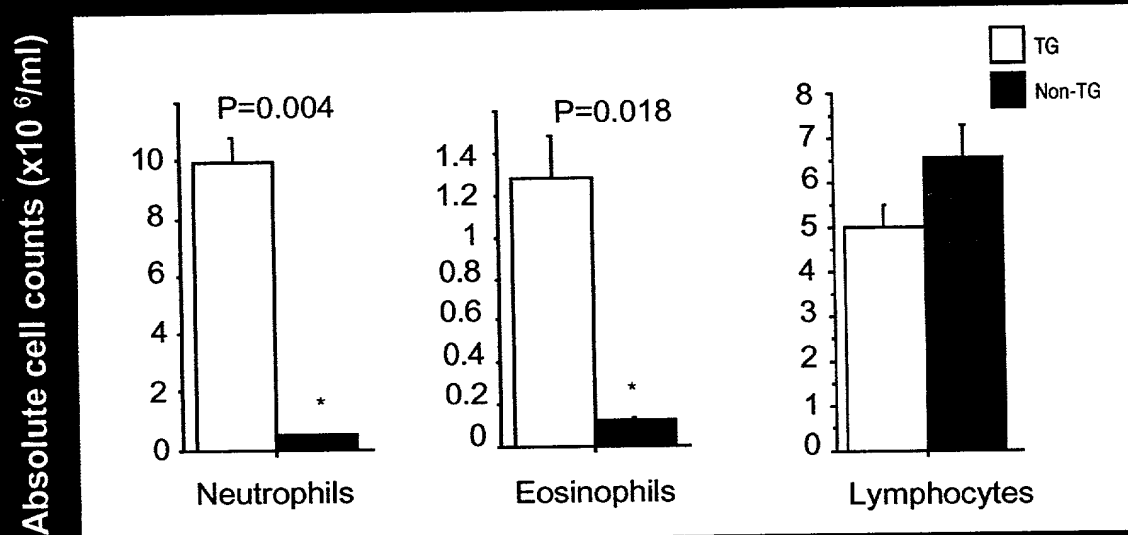


FIGURE 64

G-CSF is elevated
in mIL-17E transgenics

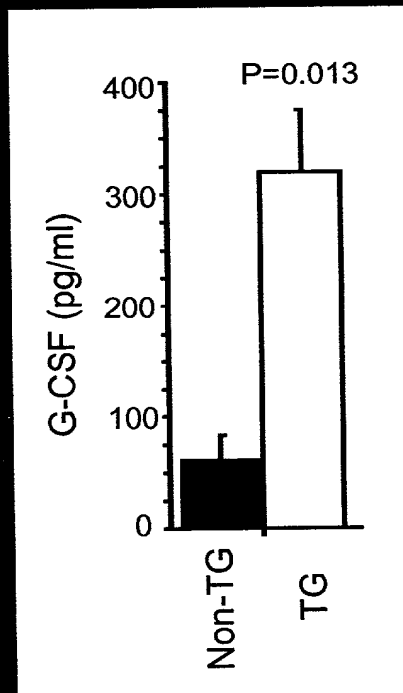


FIGURE 65

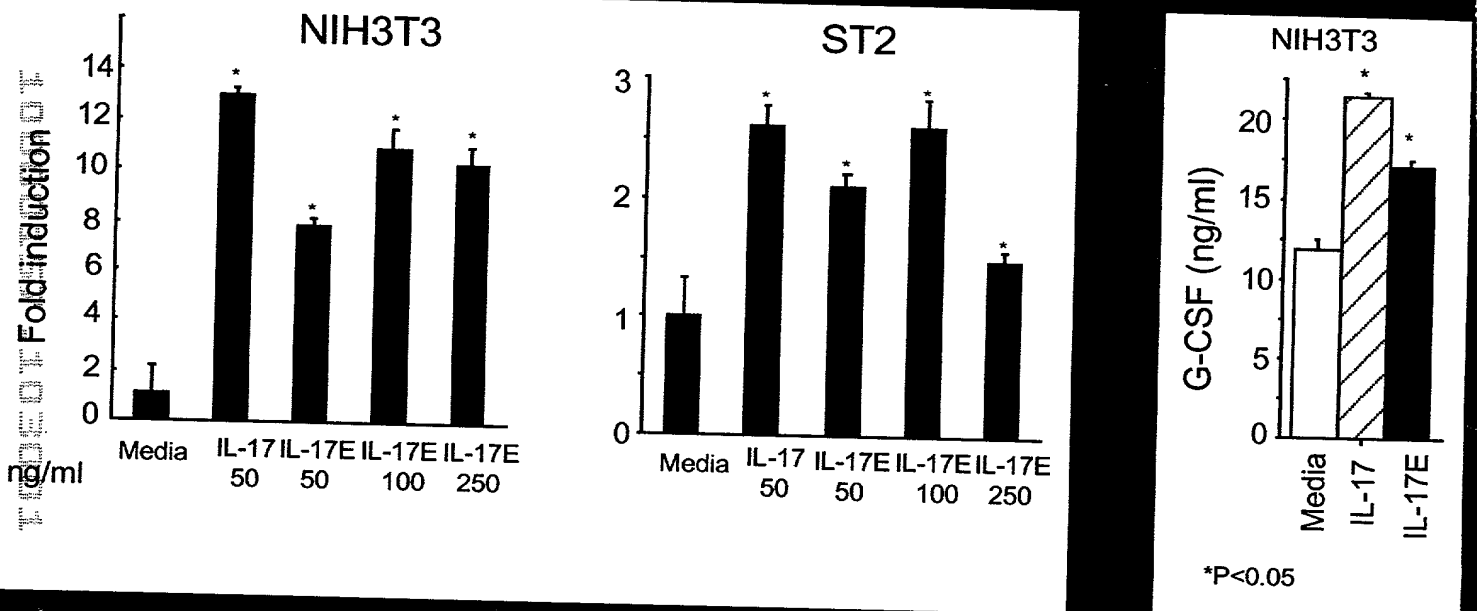
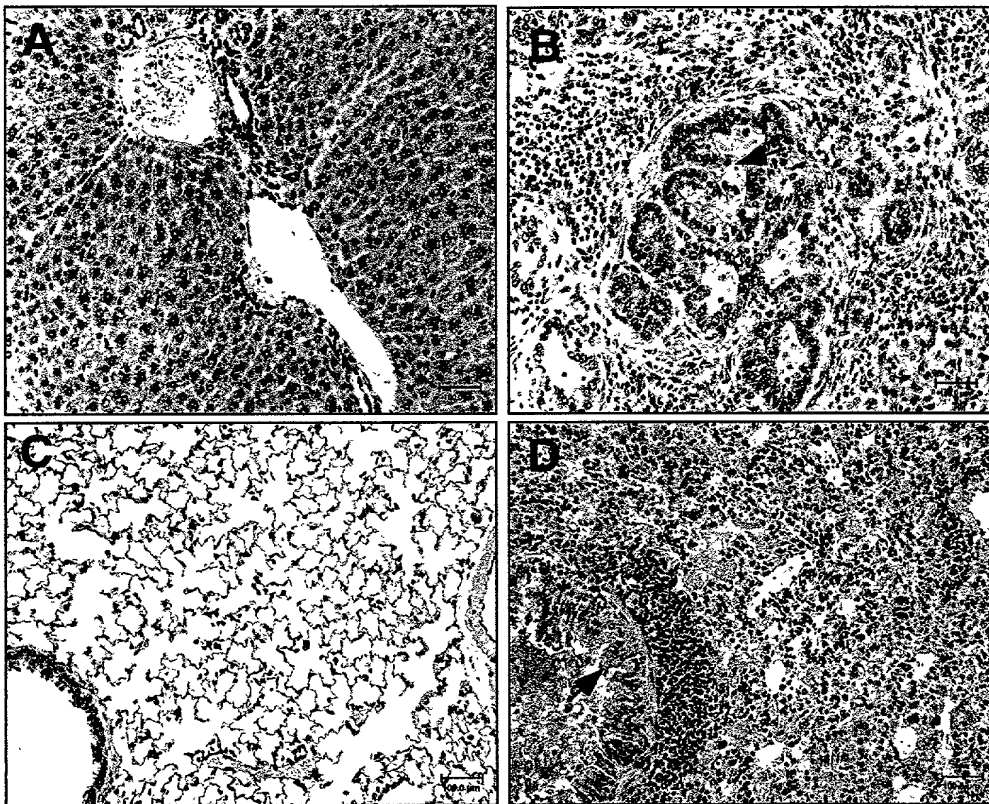


FIGURE 66



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